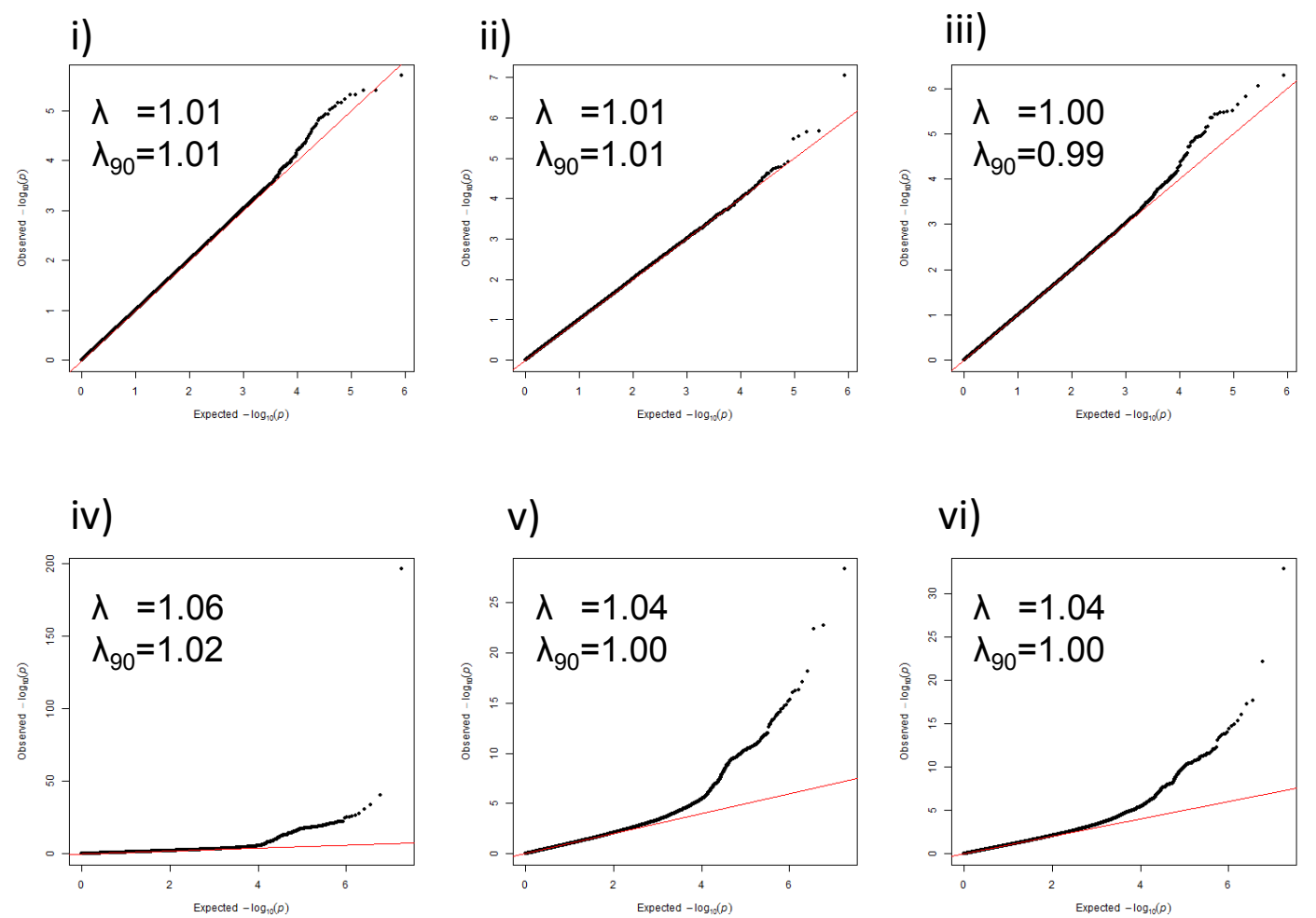


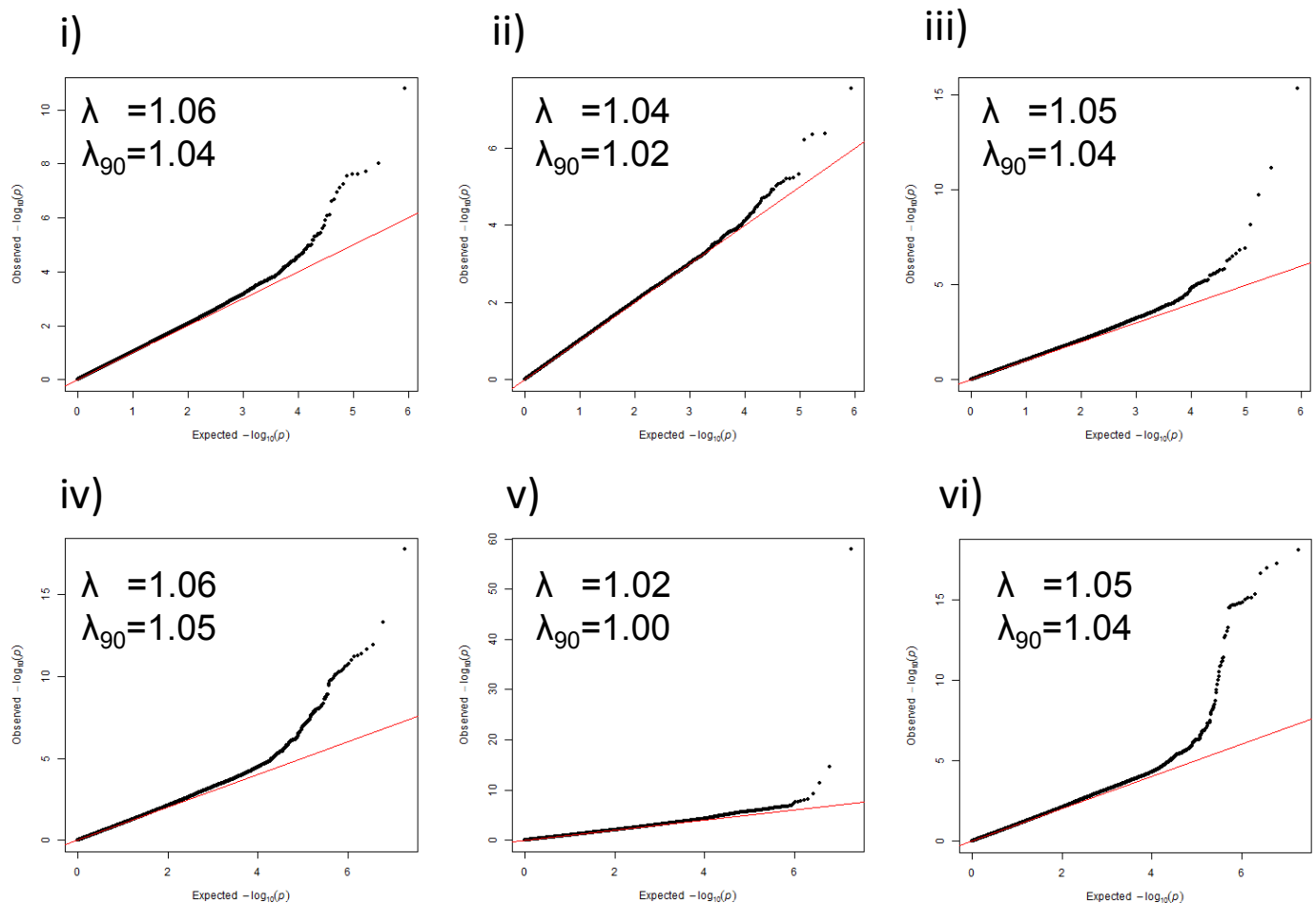
Supplementary Figure 1: QQ-plots

(a) UK-GWAS



(a) UK-GWAS i-vi (no adjustment carried out):
i) Genotyped (unadjusted) all glioma, ii) Genotyped (unadjusted) GBM, iii) Genotyped (unadjusted) non-GBM,
iv) Imputed (unadjusted) all glioma, v) Imputed (unadjusted) GBM, vi) Imputed (unadjusted) non-GBM

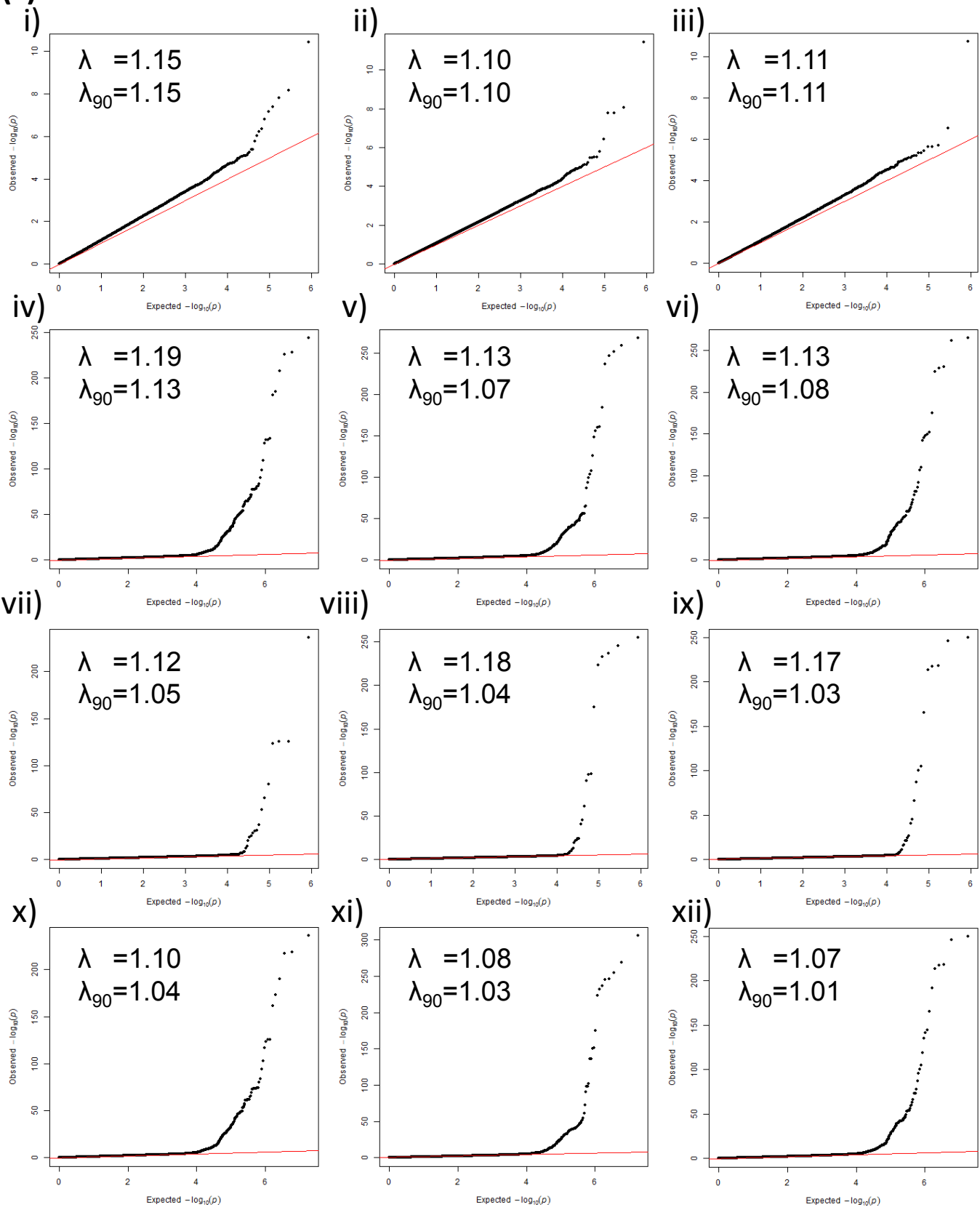
(b) French-GWAS



(b) French-GWAS i-vi (no adjustment carried out):

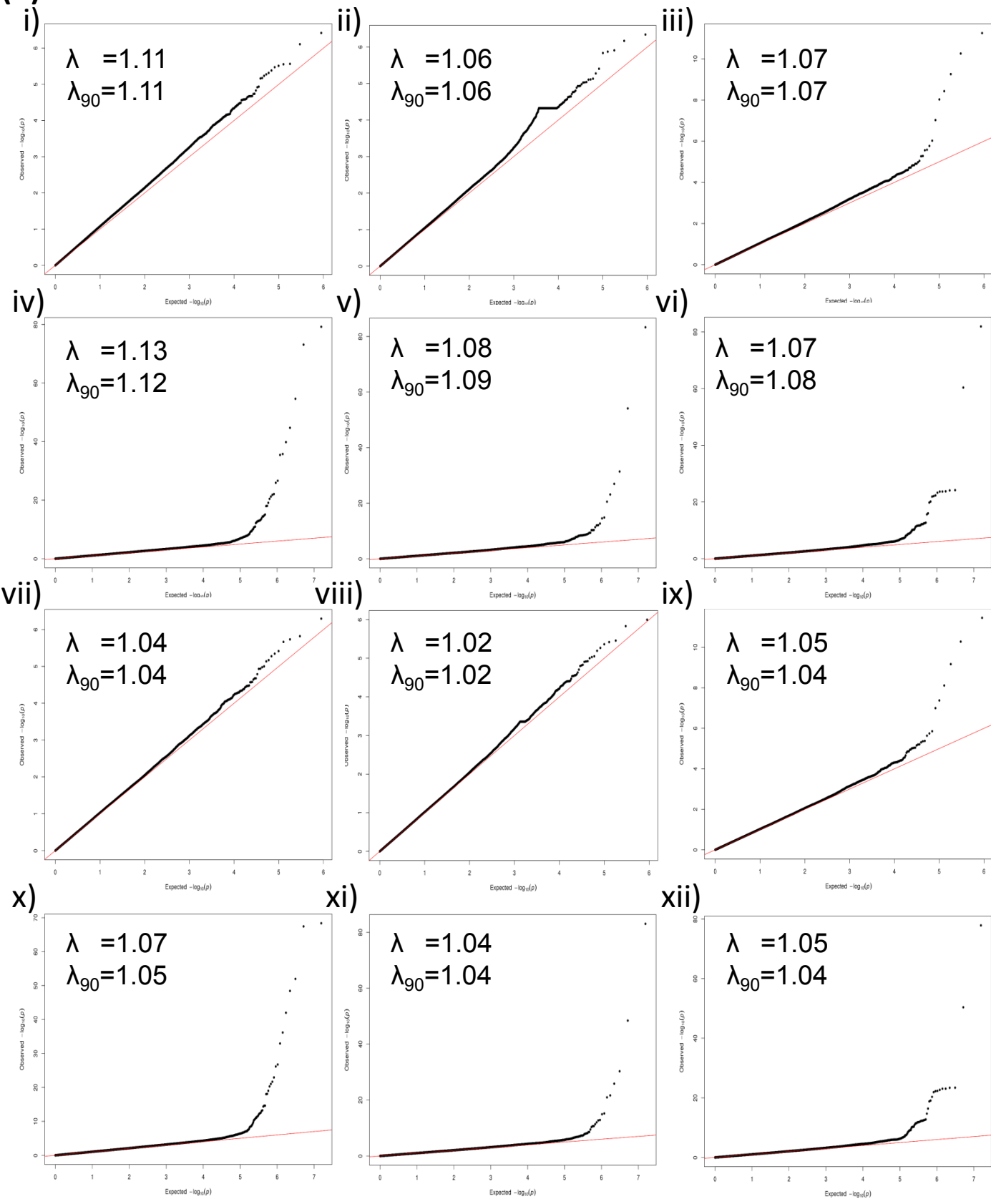
i) Genotyped (unadjusted) all glioma, ii) Genotyped (unadjusted) GBM, iii) Genotyped (unadjusted) non-GBM, iv) Imputed (unadjusted) all glioma, v) Imputed (unadjusted) GBM, vi) Imputed (unadjusted) non-GBM

(c) German-GWAS



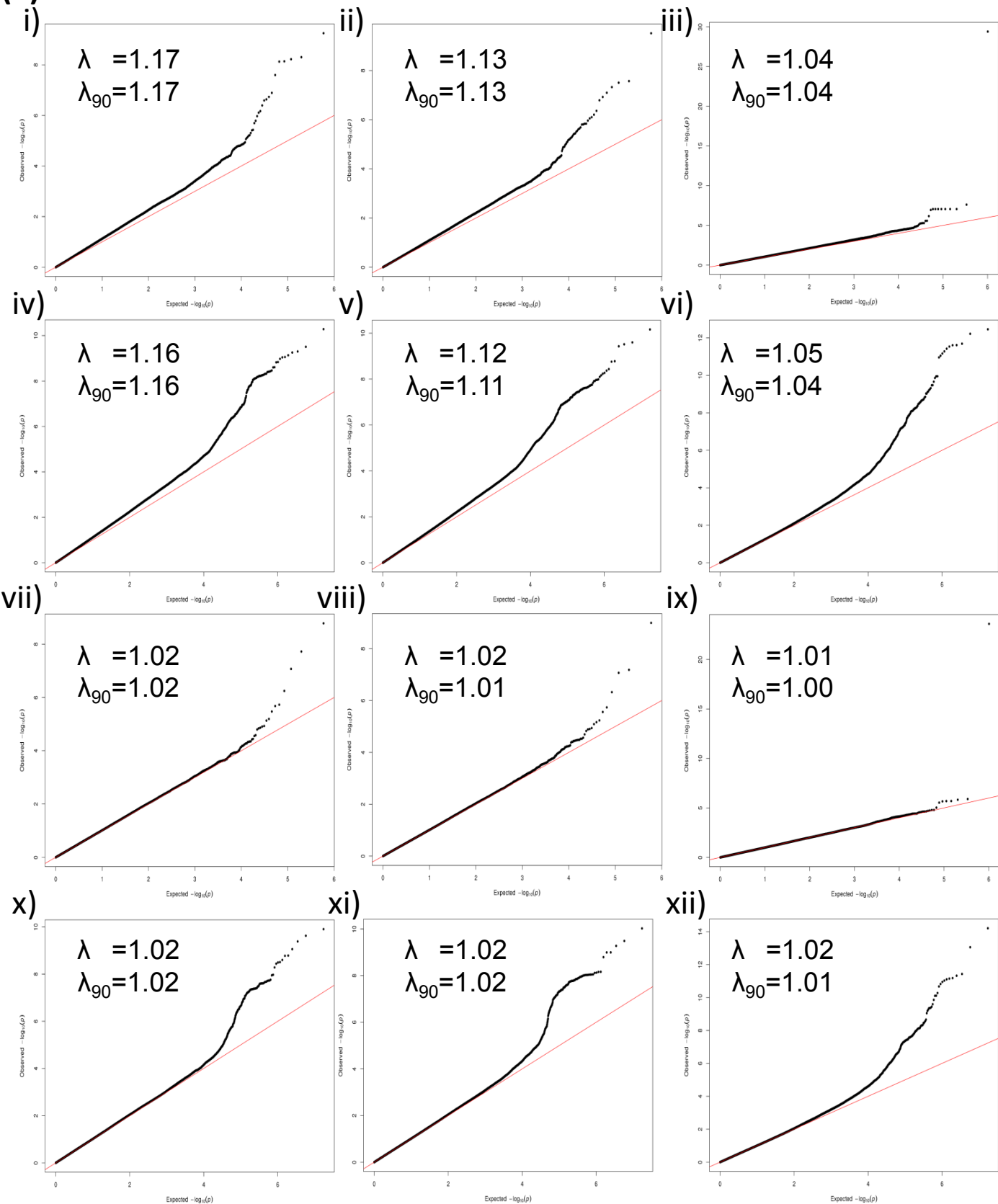
(c) German-GWAS i-xii (adjustment carried out on first ten principal components [PCs]):
i) Genotyped (unadjusted) all glioma, ii) Genotyped (unadjusted) GBM, iii) Genotyped (unadjusted) non-GBM,
iv) Imputed (unadjusted) all glioma, v) Imputed (unadjusted) GBM, vi) Imputed (unadjusted) non-GBM,
vii) Genotyped (adjusted) all glioma, viii) Genotyped (adjusted) GBM, ix) Genotyped (adjusted) non-GBM,
x) Imputed (adjusted) all glioma, xi) Imputed (adjusted) GBM, xii) Imputed (adjusted) non-GBM

(d) MDA-GWAS



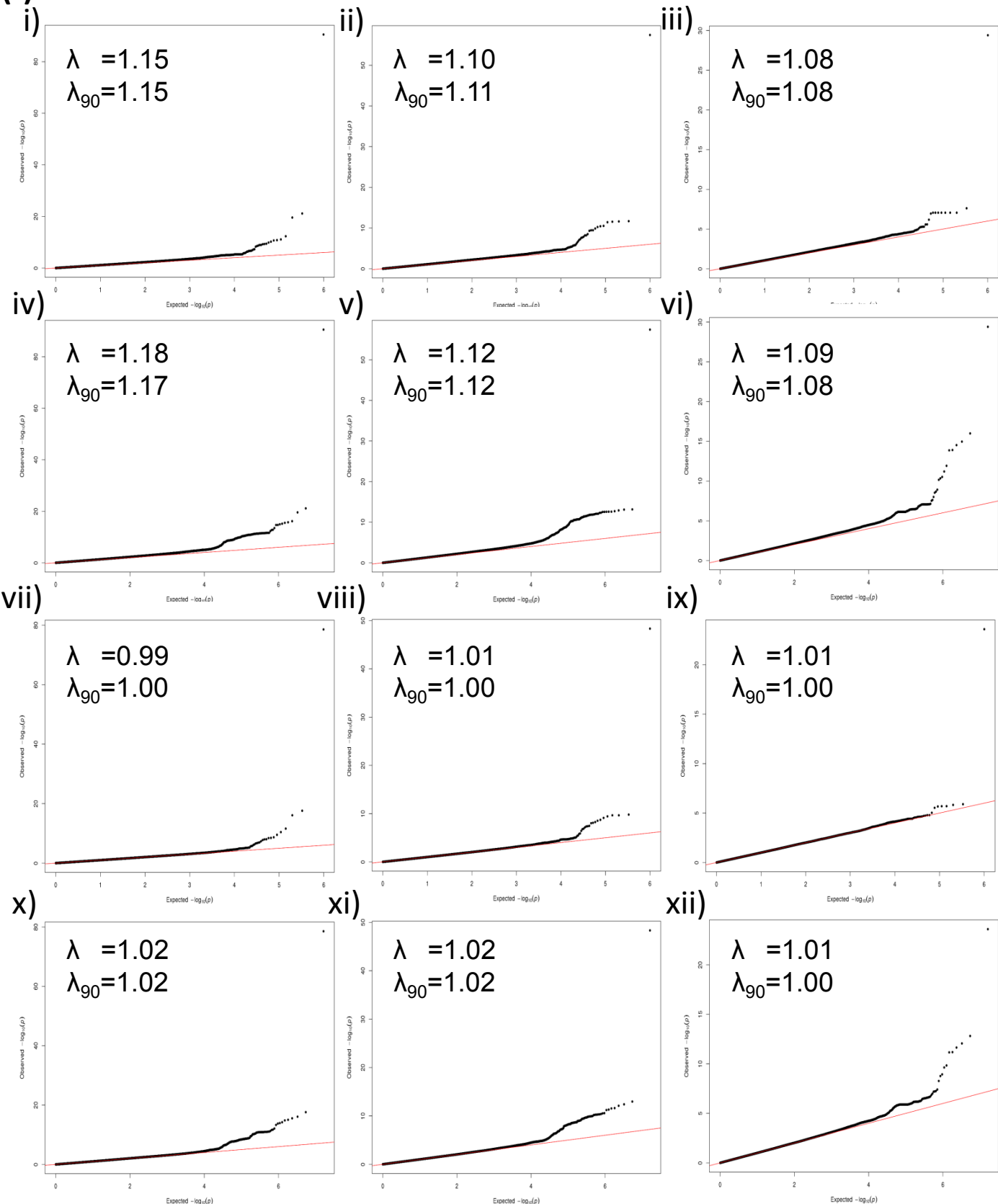
(d) MDA-GWAS i-xii: (Adjustment carried out on first two PCs)
i) Genotyped (unadjusted) all glioma, ii) Genotyped (unadjusted) GBM, iii) Genotyped (unadjusted) non-GBM,
iv) Imputed (unadjusted) all glioma, v) Imputed (unadjusted) GBM, vi) Imputed (unadjusted) non-GBM,
vii) Genotyped (adjusted) all glioma, viii) Genotyped (adjusted) GBM, ix) Genotyped (adjusted) non-GBM,
x) Imputed (adjusted) all glioma, xi) Imputed (adjusted) GBM, xii) Imputed (adjusted) non-GBM.

(e) SFAGS



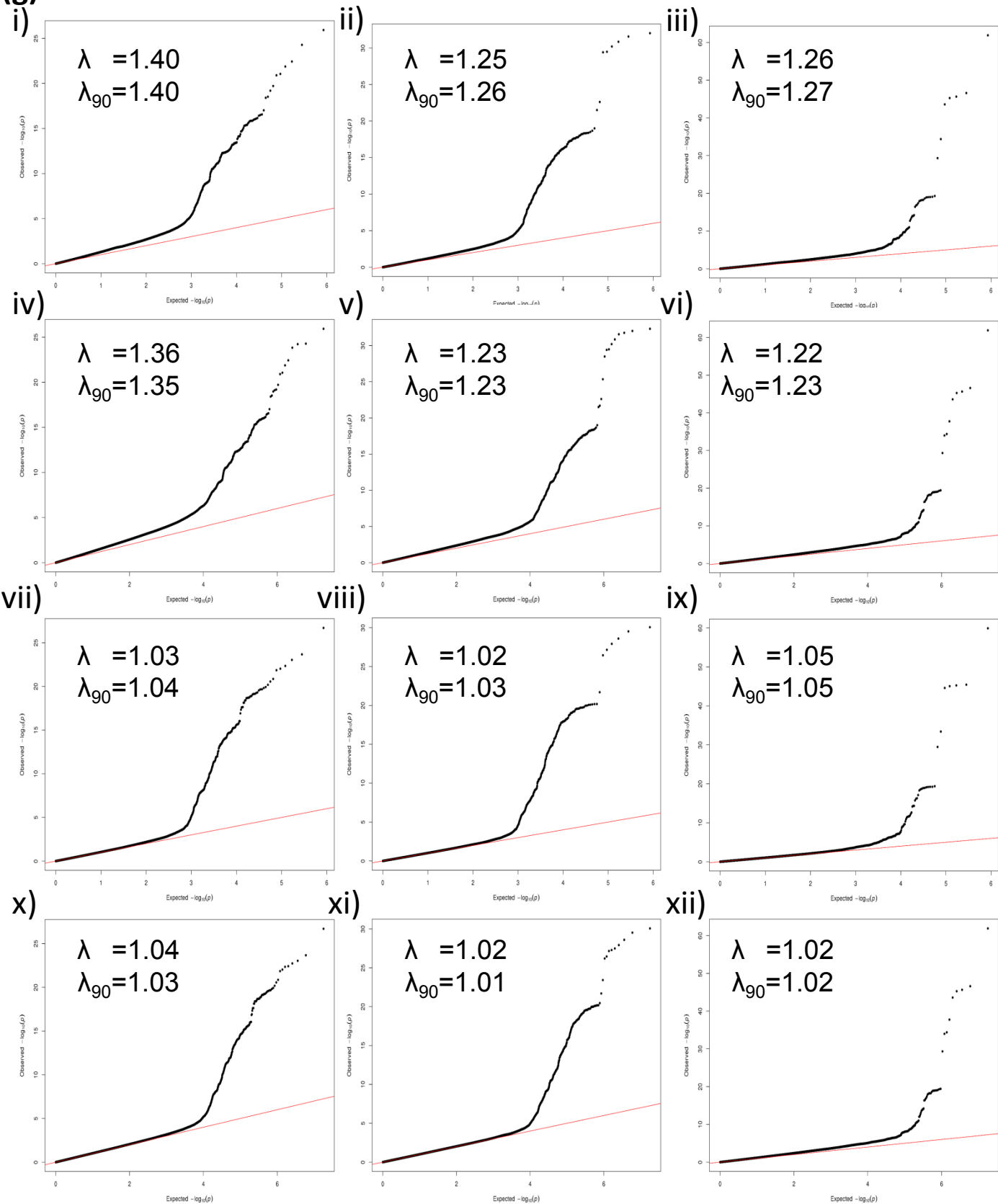
(e) SFAGS (adjustment carried out on first four PCs):
i) Genotyped (unadjusted) all glioma, ii) Genotyped (unadjusted) GBM, iii) Genotyped (unadjusted) non-GBM, iv) Imputed (unadjusted) all glioma, v) Imputed (unadjusted) GBM, vi) Imputed (unadjusted) non-GBM, vii) Genotyped (adjusted) all glioma, viii) Genotyped (adjusted) GBM, ix) Genotyped (adjusted) non-GBM, x) Imputed (adjusted) all glioma, xi) Imputed (adjusted) GBM, xii) Imputed (adjusted) non-GBM

(f) GliomaScan



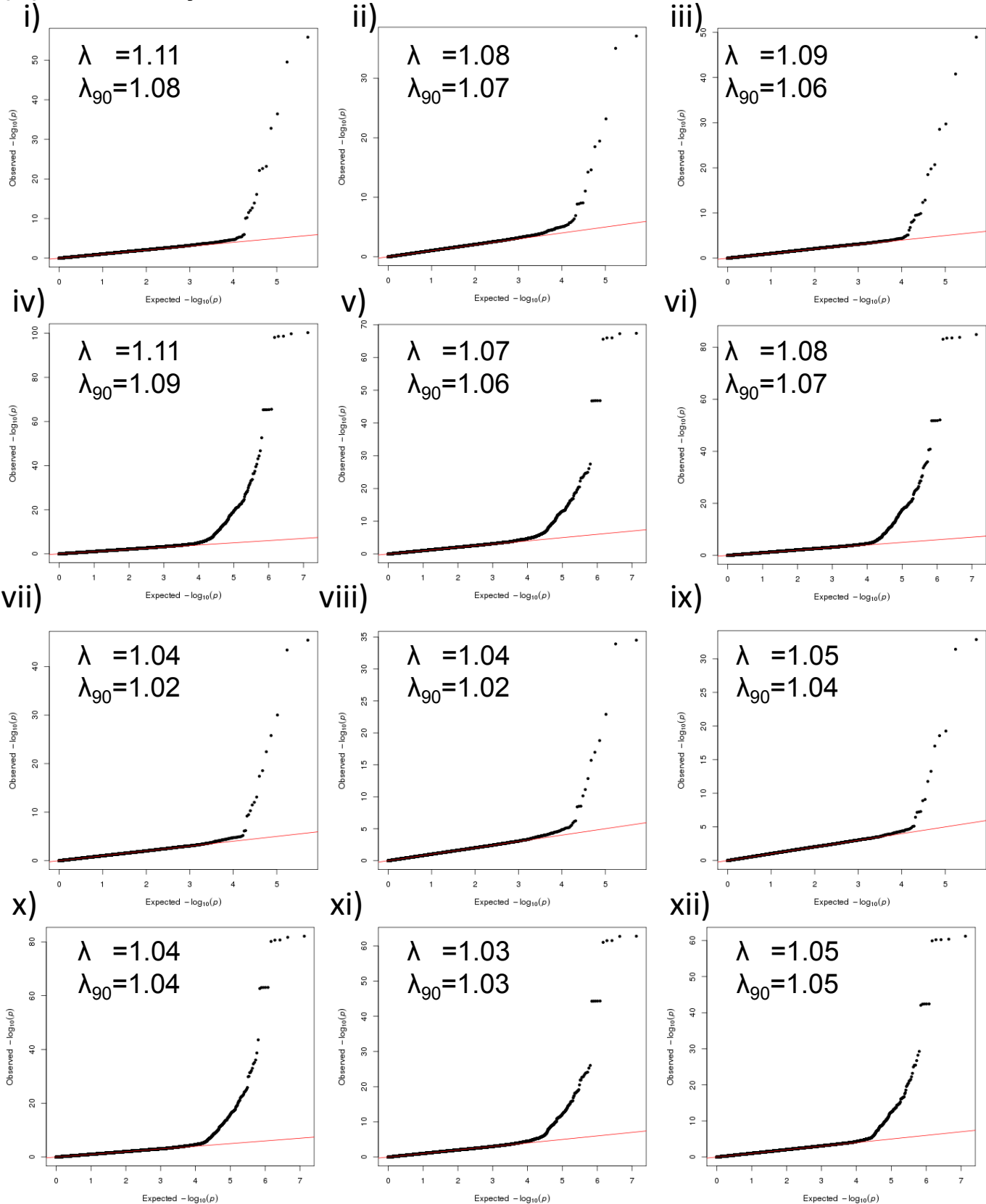
(f) GliomaScan i-xii (adjustment carried out on first four PCs):
i) Genotyped (unadjusted) all glioma, ii) Genotyped (unadjusted) GBM, iii) Genotyped (unadjusted) non-GBM, iv) Imputed (unadjusted) all glioma, v) Imputed (unadjusted) GBM, vi) Imputed (unadjusted) non-GBM, vii) Genotyped (adjusted) all glioma, viii) Genotyped (adjusted) GBM, ix) Genotyped (adjusted) non-GBM, x) Imputed (adjusted) all glioma, xi) Imputed (adjusted) GBM, xii) Imputed (adjusted) non-GBM

(g) GICC



(g) GICC (adjustment carried out on first two PCs):
i) Genotyped (unadjusted) all glioma, ii) Genotyped (unadjusted) GBM, iii) Genotyped (unadjusted) non-GBM,
iv) Imputed (unadjusted) all glioma, v) Imputed (unadjusted) GBM, vi) Imputed (unadjusted) non-GBM,
vii) Genotyped (adjusted) all glioma, viii) Genotyped (adjusted) GBM, ix) Genotyped (adjusted) non-GBM,
x) Imputed (adjusted) all glioma, xi) Imputed (adjusted) GBM, xii) Imputed (adjusted) non-GBM

(h) UCSF/Mayo

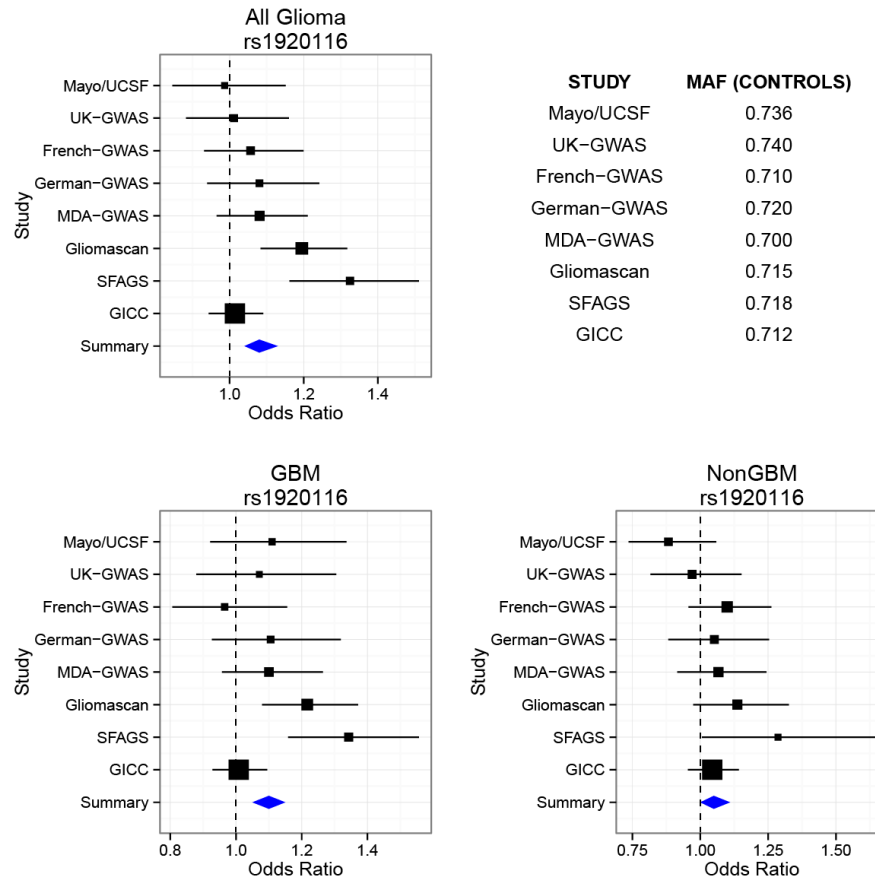


(h) UCSF/Mayo i-xii (adjustment carried out on age, gender, first three PCs):
i) Genotyped (unadjusted) all glioma, ii) Genotyped (unadjusted) GBM, iii) Genotyped (unadjusted) non-GBM,
iv) Imputed (unadjusted) all glioma, v) Imputed (unadjusted) GBM, vi) Imputed (unadjusted) non-GBM,
vii) Genotyped (adjusted) all glioma, viii) Genotyped (adjusted) GBM, ix) Genotyped (adjusted) non-GBM,
x) Imputed (adjusted) all glioma, xi) Imputed (adjusted) GBM, xii) Imputed (adjusted) non-GBM

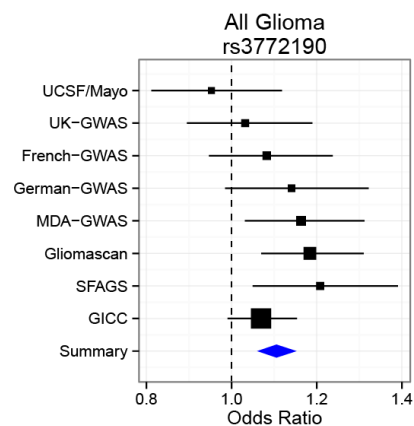
Supplementary Figure 2: Forest plots of effect size and direction for the SNPs from newly reported and previously reported loci associated with glioma risk.

Previously reported glioma risk loci

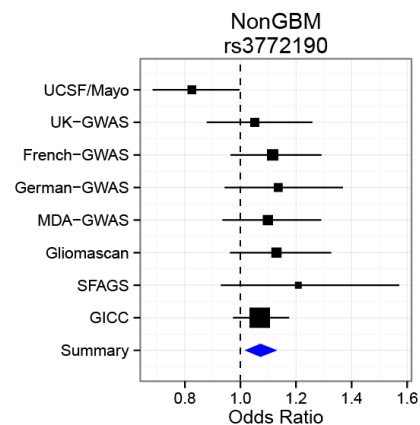
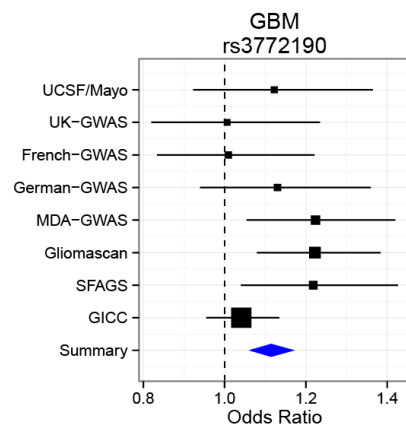
rs1920116 (3q26.2)



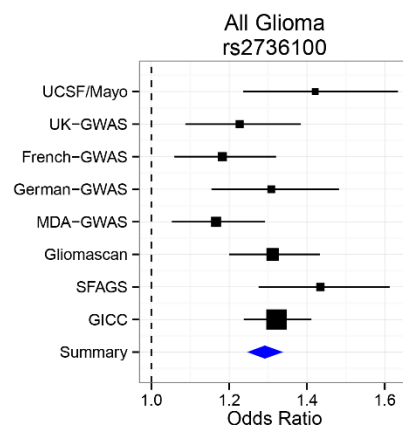
rs3772190 (3q26.2)



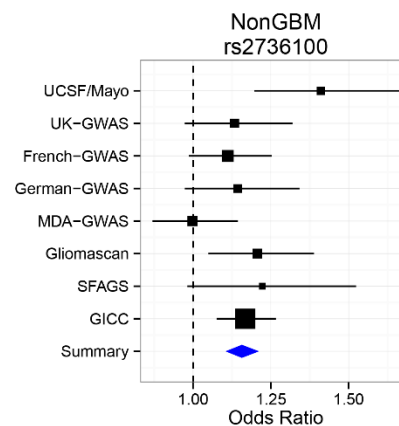
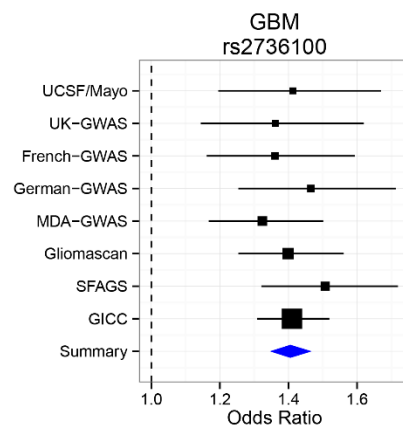
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.771
UK-GWAS	0.755
French-GWAS	0.774
German-GWAS	0.747
MDA-GWAS	0.756
Gliomascan	0.742
SFAGS	0.762
GICC	0.754



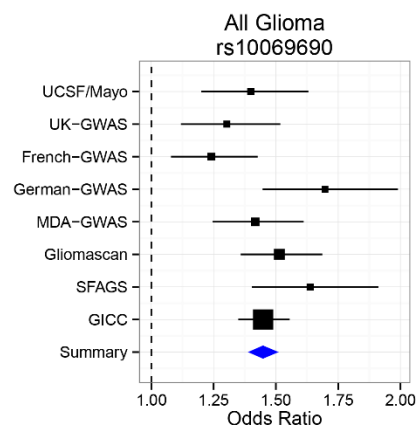
rs2736100 (5p15.33)



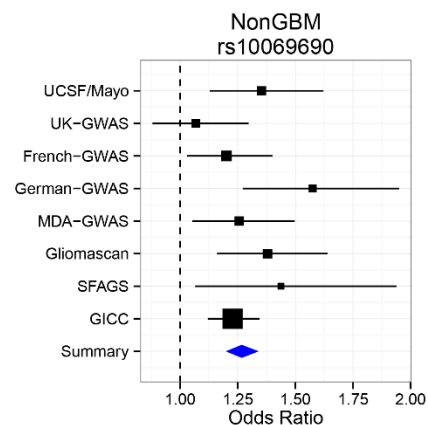
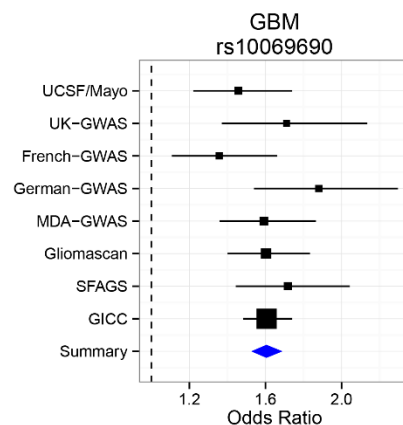
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.502
UK-GWAS	0.514
French-GWAS	0.520
German-GWAS	0.500
MDA-GWAS	0.508
Gliomascan	0.504
SFAGS	0.504
GICC	0.506



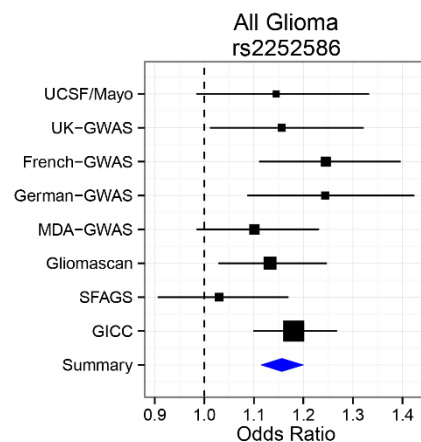
rs10069690 (5p15.33)



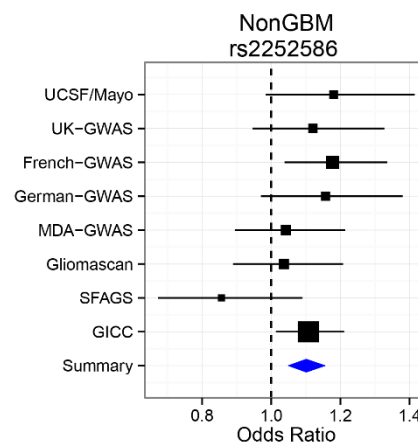
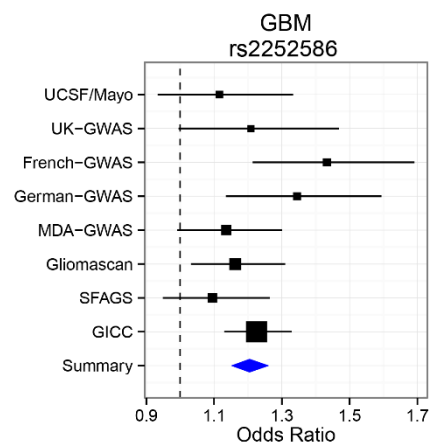
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.273
UK-GWAS	0.264
French-GWAS	0.268
German-GWAS	0.244
MDA-GWAS	0.255
Gliomascan	0.268
SFAGS	0.259
GICC	0.264



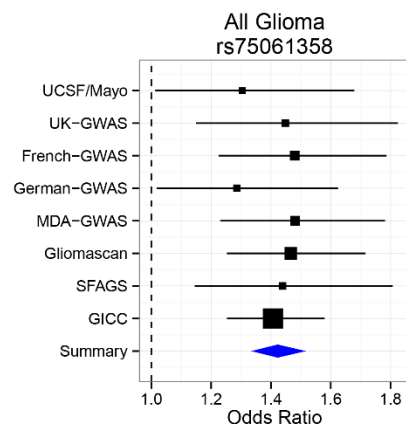
rs2252586 (7p11.2)



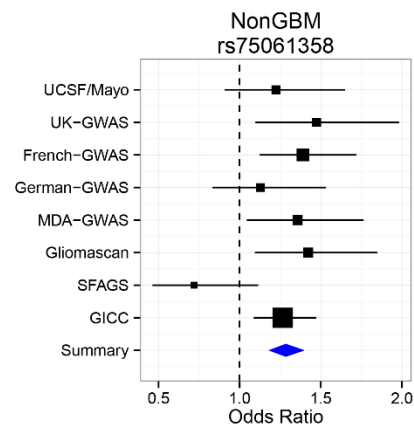
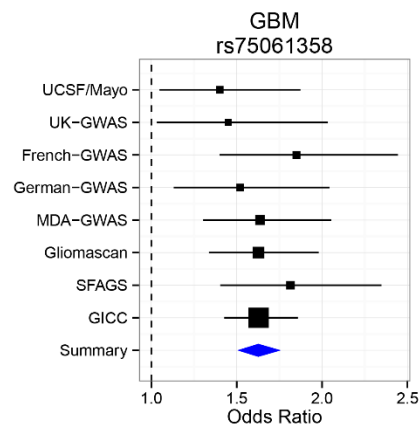
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.287
UK-GWAS	0.296
French-GWAS	0.304
German-GWAS	0.298
MDA-GWAS	0.297
Gliomascan	0.292
SFAGS	0.297
GICC	0.278



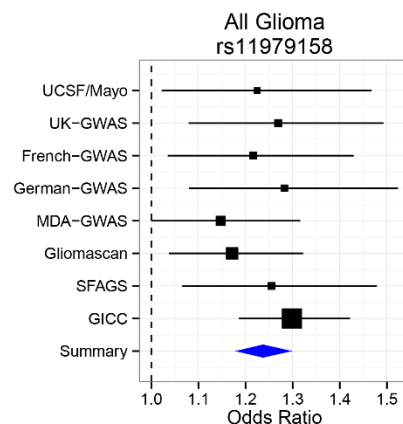
rs75061358 (7p11.2)



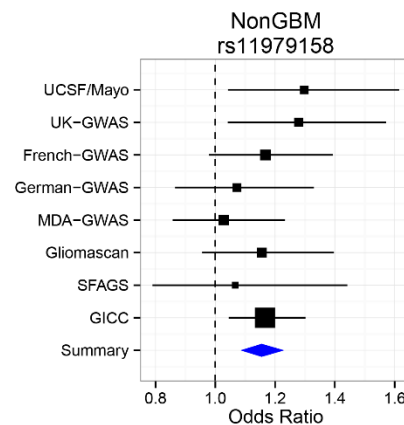
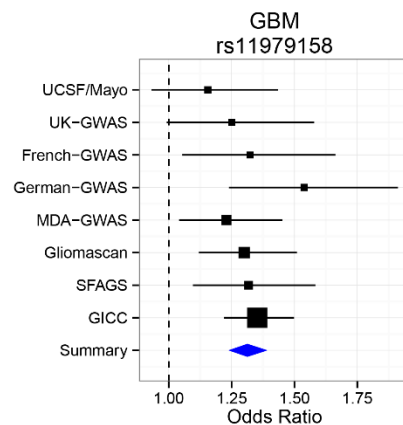
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.078
UK-GWAS	0.077
French-GWAS	0.083
German-GWAS	0.082
MDA-GWAS	0.080
Gliomascan	0.082
SFAGS	0.082
GICC	0.076



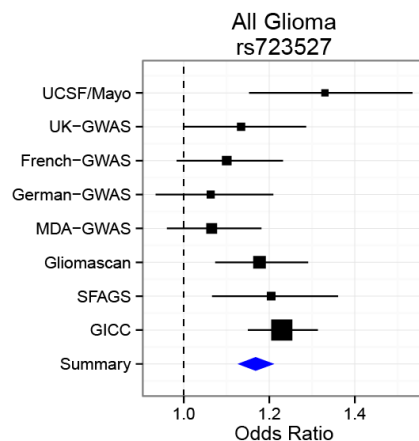
rs11979158 (7p11.2)



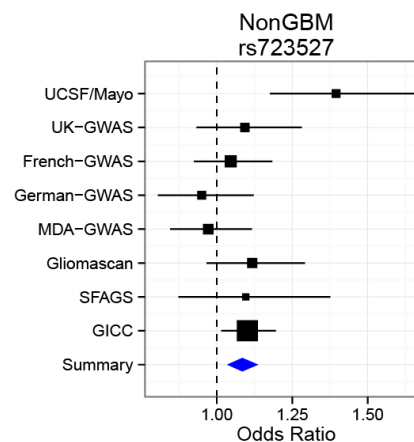
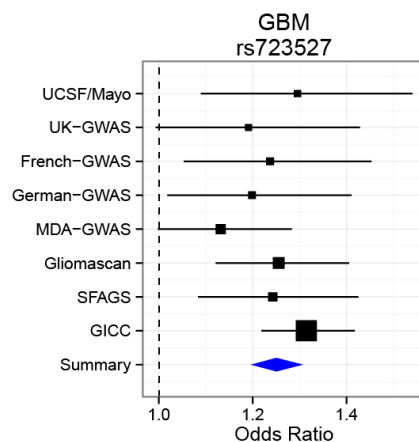
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.816
UK-GWAS	0.825
French-GWAS	0.853
German-GWAS	0.823
MDA-GWAS	0.834
Gliomascan	0.832
SFAGS	0.849
GICC	0.824



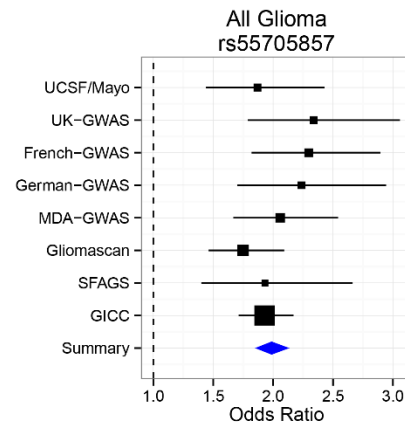
rs723527 (7p11.2)



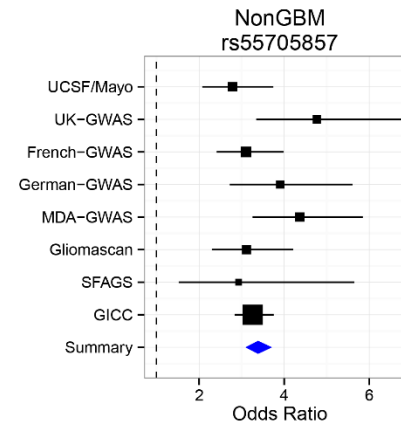
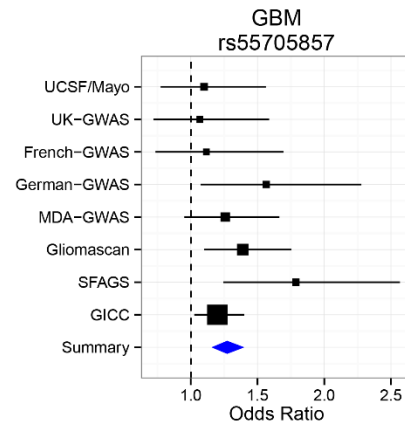
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.568
UK-GWAS	0.588
French-GWAS	0.621
German-GWAS	0.603
MDA-GWAS	0.595
Gliomascan	0.598
SFAGS	0.605
GICC	0.573



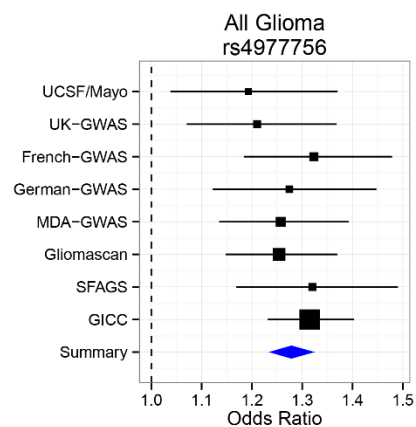
rs55705857 (8q24.21)



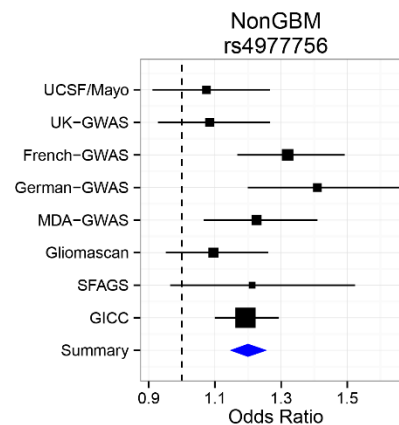
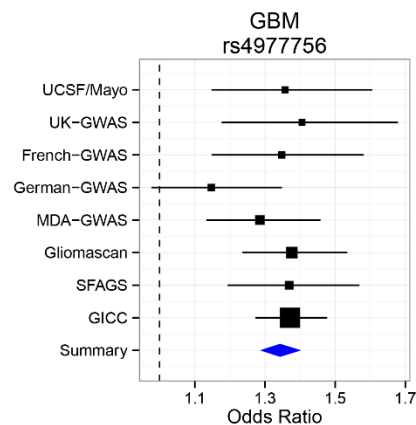
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.066
UK-GWAS	0.065
French-GWAS	0.049
German-GWAS	0.058
MDA-GWAS	0.067
Gliomascan	0.067
SFAGS	0.051
GICC	0.056



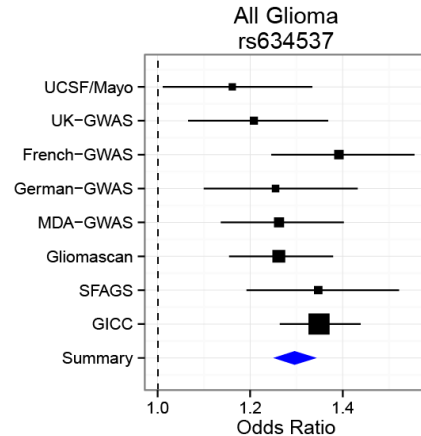
rs4977756 (9p21.3)



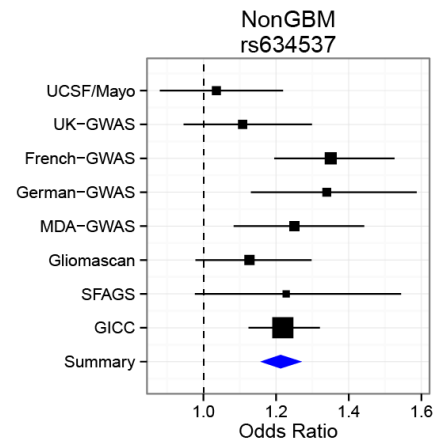
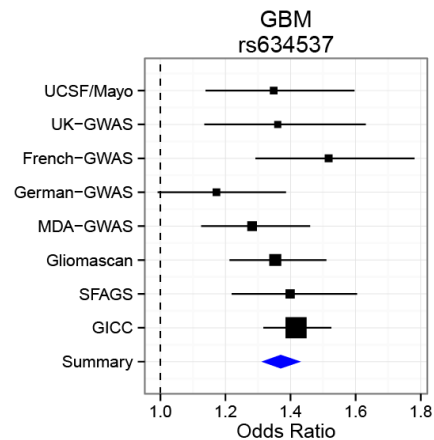
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.577
UK-GWAS	0.588
French-GWAS	0.657
German-GWAS	0.571
MDA-GWAS	0.592
Gliomascan	0.587
SFAGS	0.629
GICC	0.589



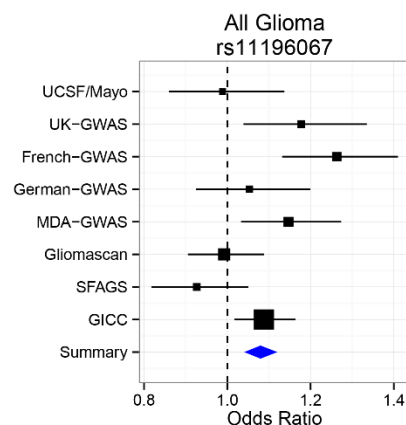
rs634537 (9p21.3)



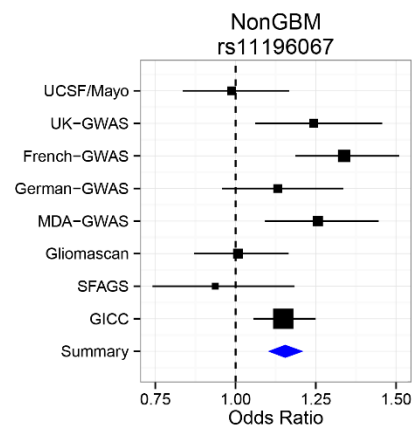
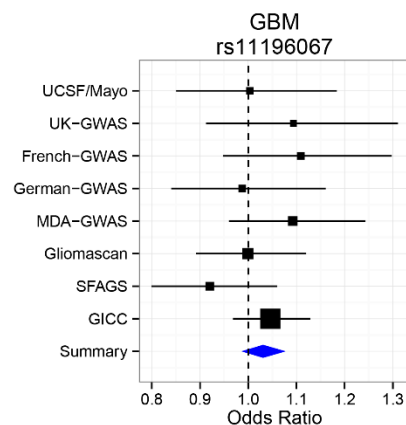
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.449
UK-GWAS	0.426
French-GWAS	0.358
German-GWAS	0.420
MDA-GWAS	0.413
Gliomascan	0.428
SFAGS	0.389
GICC	0.427



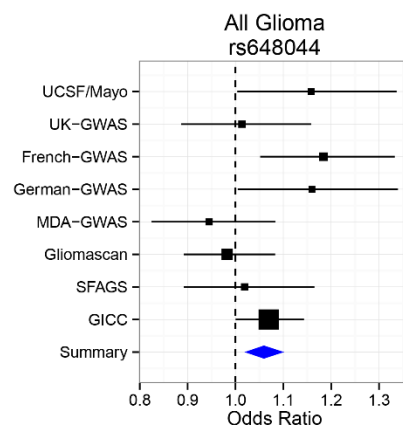
rs11196067 (10q25.2)



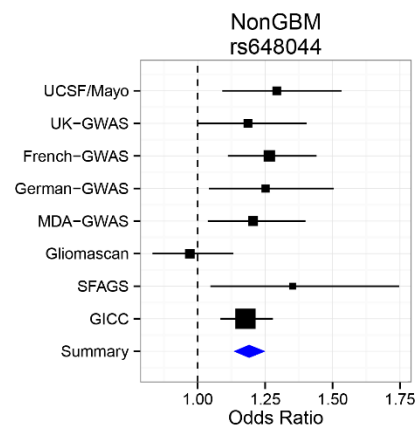
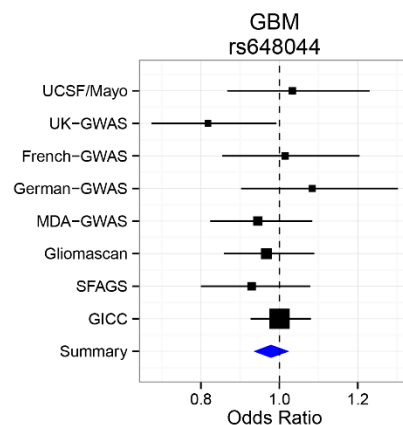
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.600
UK-GWAS	0.593
French-GWAS	0.555
German-GWAS	0.603
MDA-GWAS	0.601
Gliomascan	0.599
SFAGS	0.609
GICC	0.584



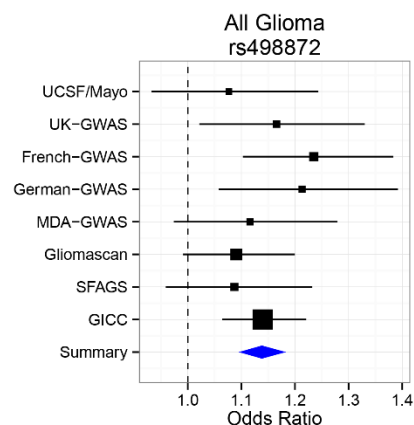
rs648044 (11q23.2)



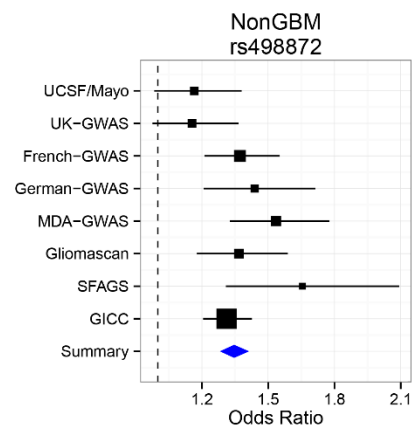
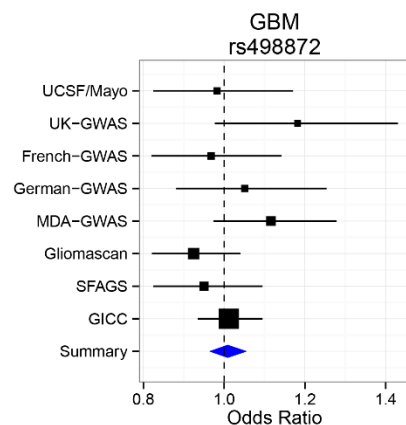
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.620
UK-GWAS	0.596
French-GWAS	0.644
German-GWAS	0.641
MDA-GWAS	0.615
Gliomascan	0.609
SFAGS	0.628
GICC	0.608



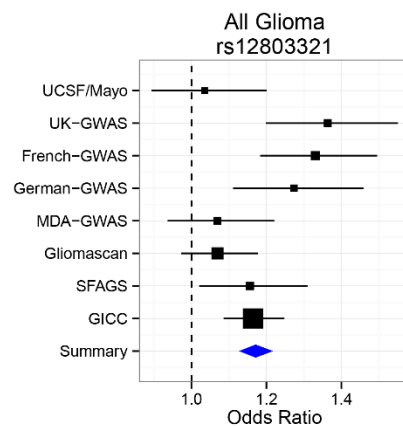
rs498872 (11q23.3)



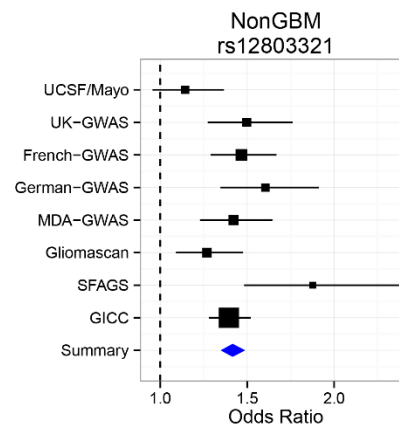
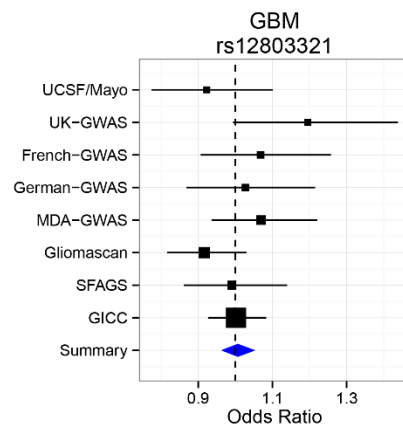
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.678
UK-GWAS	0.686
French-GWAS	0.675
German-GWAS	0.699
MDA-GWAS	0.692
Gliomascan	0.691
SFAGS	0.694
GICC	0.693



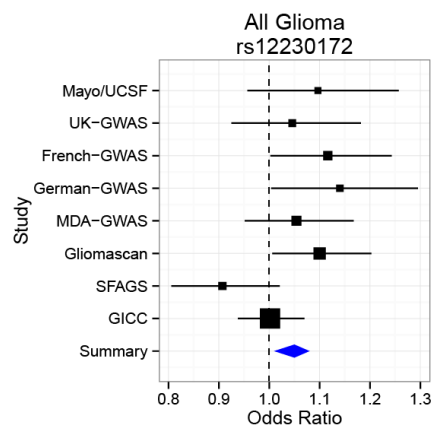
rs12803321 (11q23.3)



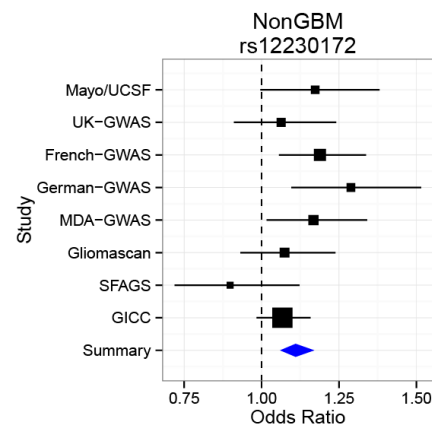
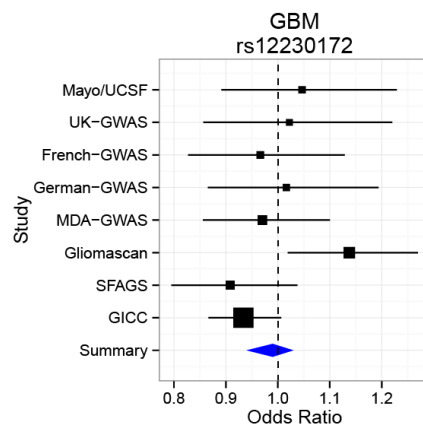
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.658
UK-GWAS	0.640
French-GWAS	0.649
German-GWAS	0.664
MDA-GWAS	0.652
Gliomascan	0.657
SFAGS	0.639
GICC	0.660



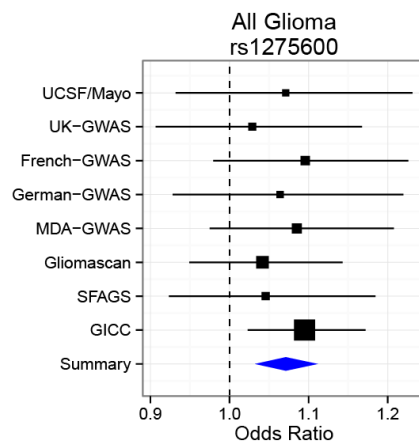
rs12230172 (12q21.2)



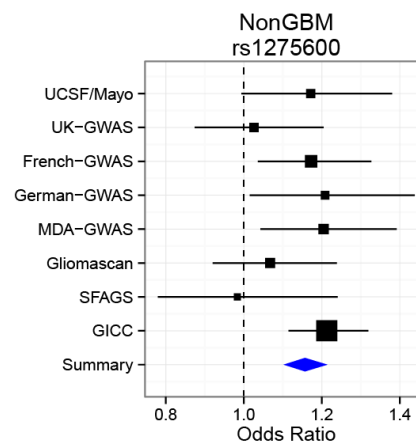
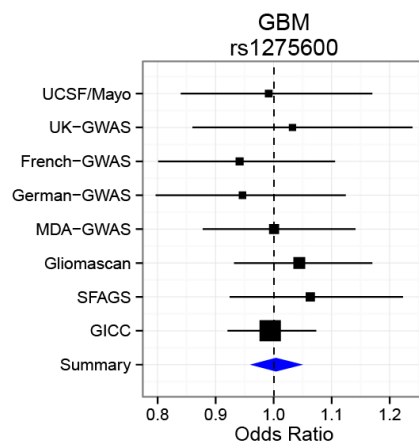
STUDY	MAF (CONTROLS)
Mayo/UCSF	0.529
UK-GWAS	0.500
French-GWAS	0.478
German-GWAS	0.457
MDA-GWAS	0.457
Gliomascan	0.458
SFAGS	0.447
GICC	0.450



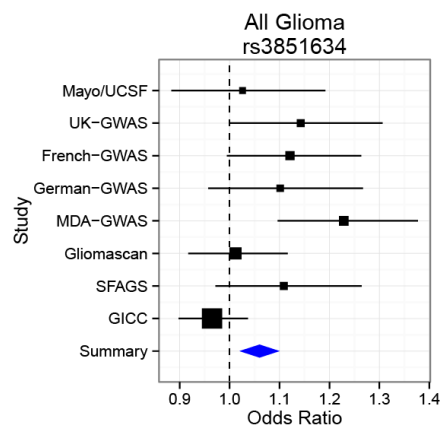
rs1275600 (12q21.2)



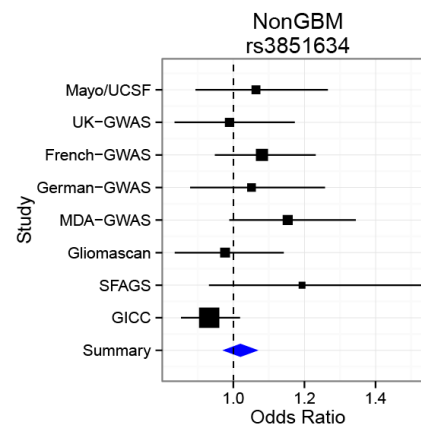
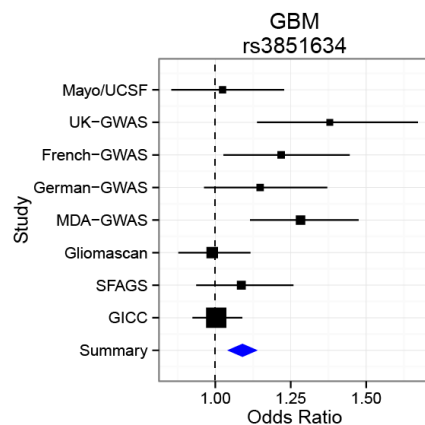
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.609
UK-GWAS	0.616
French-GWAS	0.586
German-GWAS	0.627
MDA-GWAS	0.619
Gliomascan	0.632
SFAGS	0.610
GICC	0.611



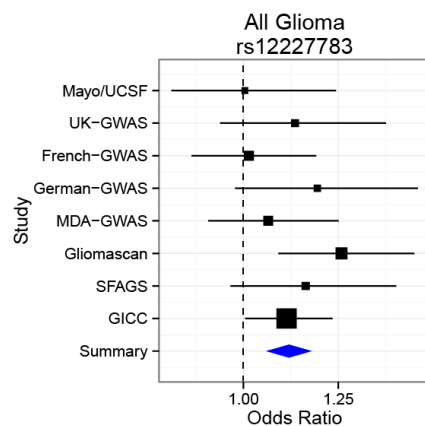
rs3851634 (12q23.33)



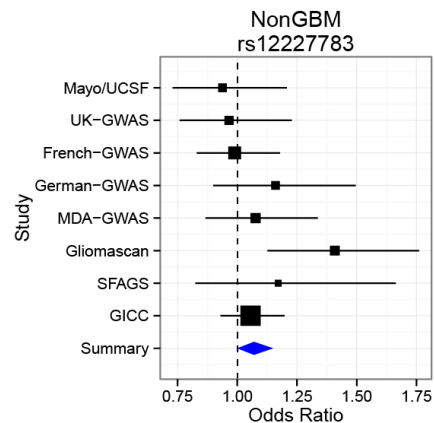
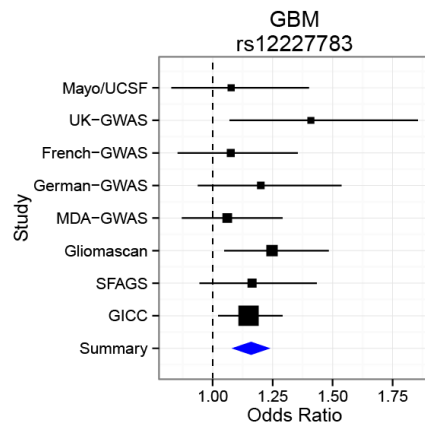
STUDY	MAF (CONTROLS)
Mayo/UCSF	0.711
UK-GWAS	0.705
French-GWAS	0.692
German-GWAS	0.711
MDA-GWAS	0.713
Gliomascan	0.711
SFAGS	0.698
GICC	0.717



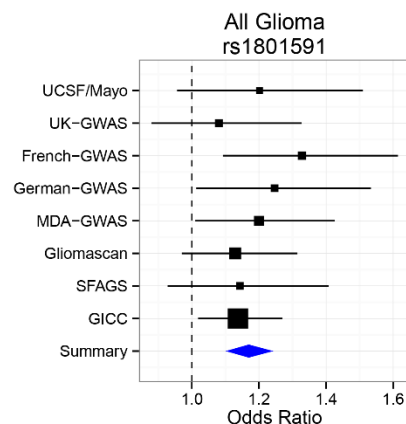
rs12227783 (12q23.33)



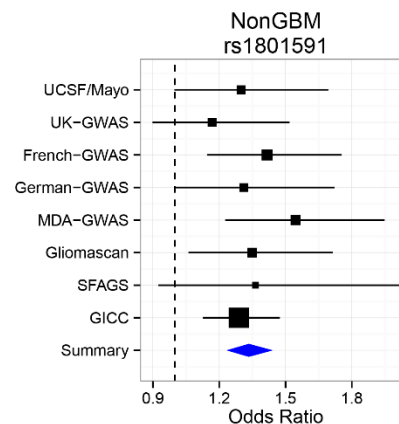
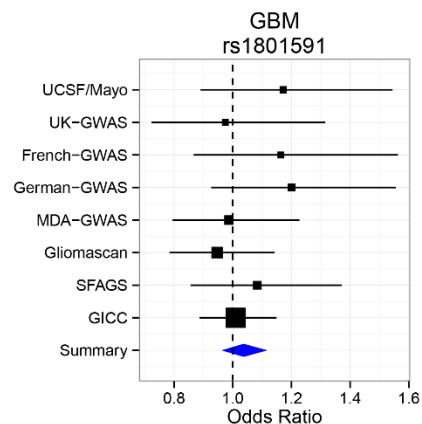
STUDY	MAF (CONTROLS)
Mayo/UCSF	0.886
UK-GWAS	0.869
French-GWAS	0.877
German-GWAS	0.879
MDA-GWAS	0.877
Gliomascan	0.877
SFAGS	0.886
GICC	0.881



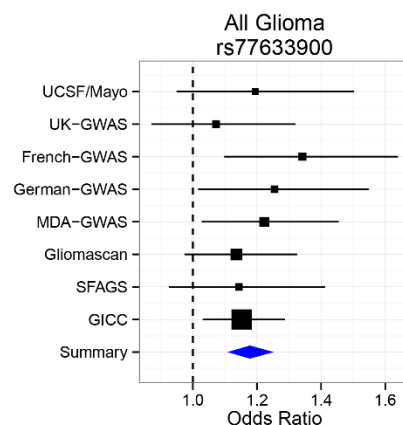
rs1801591 (15q24.2)



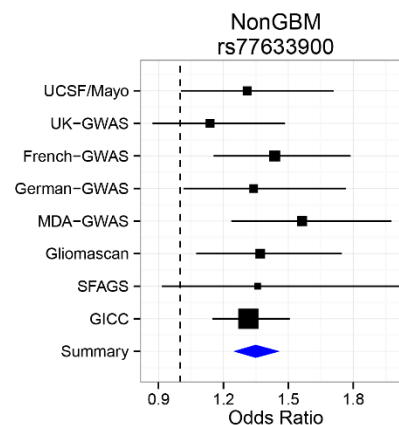
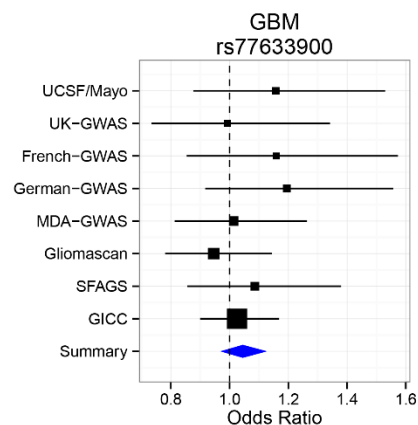
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.092
UK-GWAS	0.093
French-GWAS	0.073
German-GWAS	0.098
MDA-GWAS	0.091
Gliomascan	0.090
SFAGS	0.083
GICC	0.097



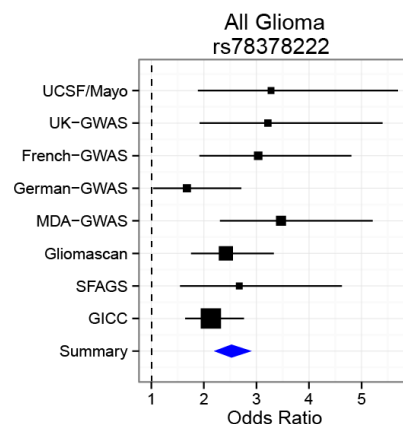
rs77633900 (15q24.2)



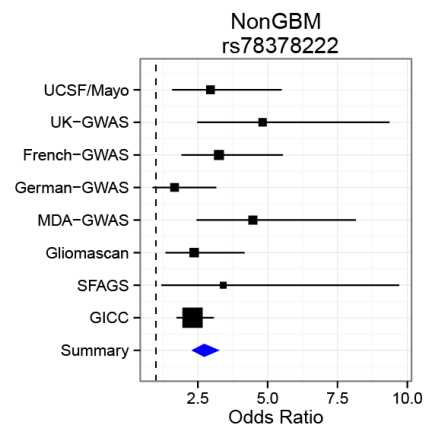
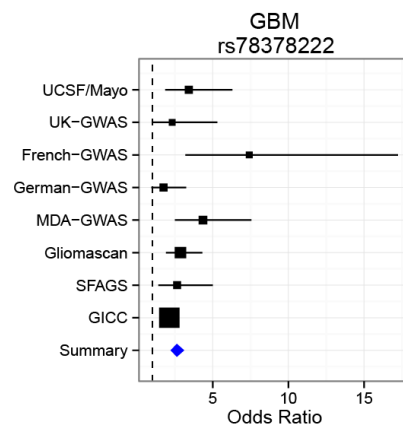
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.090
UK-GWAS	0.091
French-GWAS	0.069
German-GWAS	0.096
MDA-GWAS	0.088
Gliomascan	0.088
SFAGS	0.081
GICC	0.094



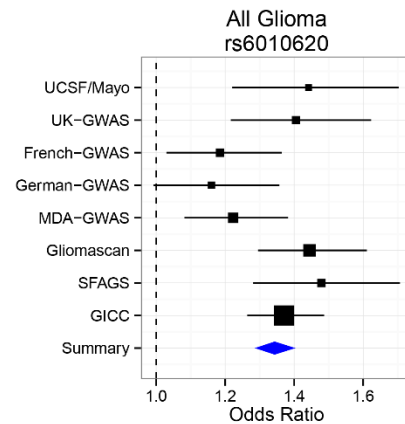
rs78378222 (17p13.1)



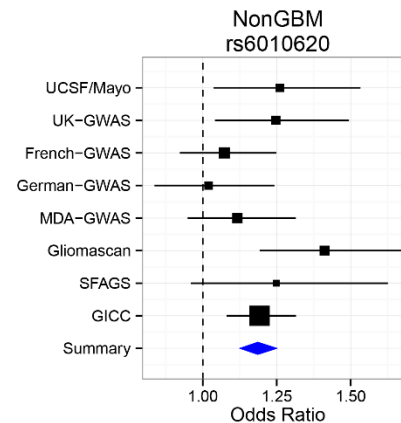
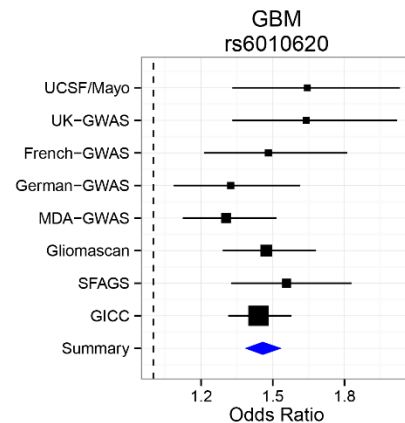
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.011
UK-GWAS	0.013
French-GWAS	0.006
German-GWAS	0.016
MDA-GWAS	0.010
Gliomascan	0.013
SFAGS	0.012
GICC	0.015



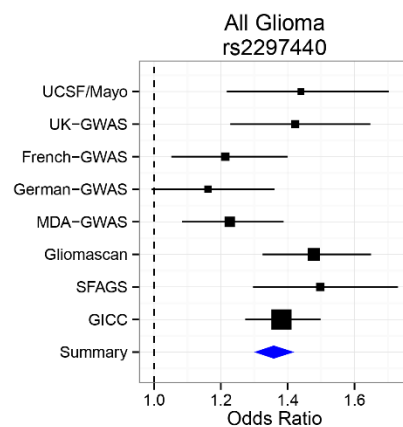
rs6010620 (20q13.33)



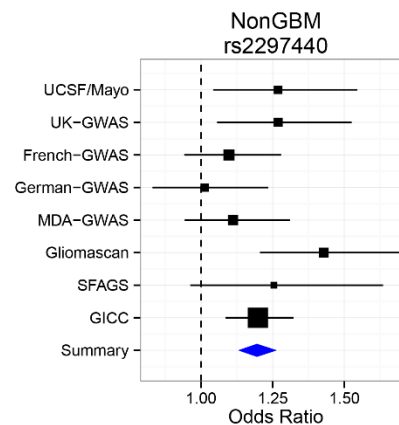
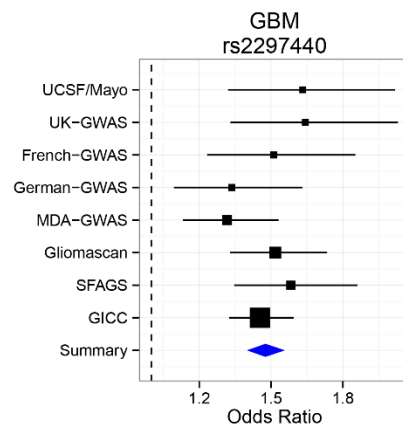
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.246
UK-GWAS	0.244
French-GWAS	0.199
German-GWAS	0.221
MDA-GWAS	0.231
Gliomascan	0.235
SFAGS	0.227
GICC	0.231



rs2297440 (20q13.33)

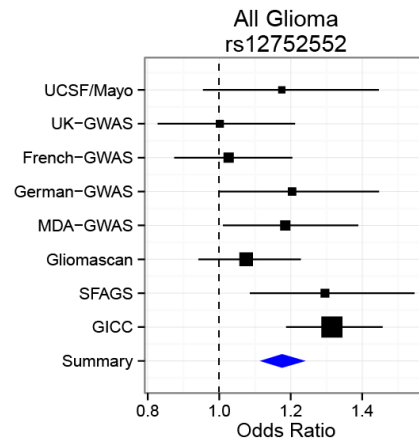


STUDY	MAF (CONTROLS)
UCSF/Mayo	0.242
UK-GWAS	0.238
French-GWAS	0.196
German-GWAS	0.219
MDA-GWAS	0.226
Gliomascan	0.234
SFAGS	0.224
GICC	0.228

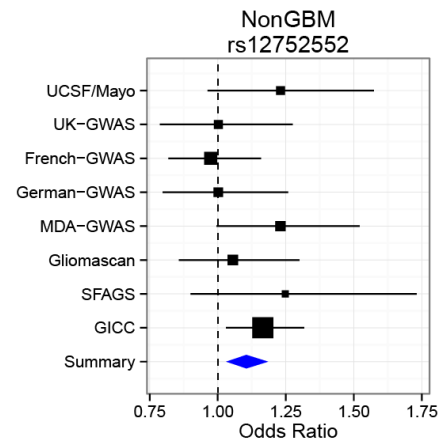
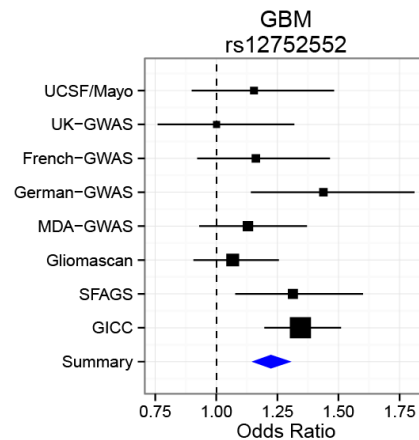


Newly reported glioma risk loci

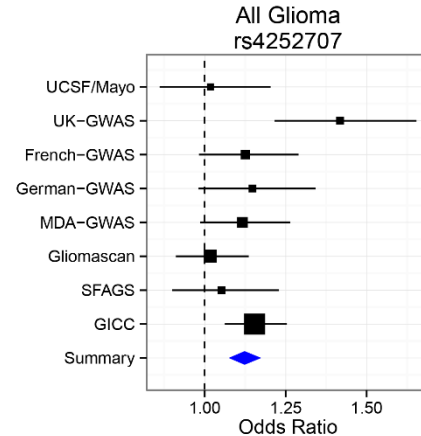
rs12752552 (1p31.3)



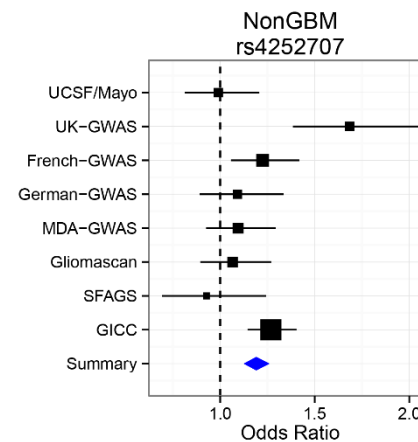
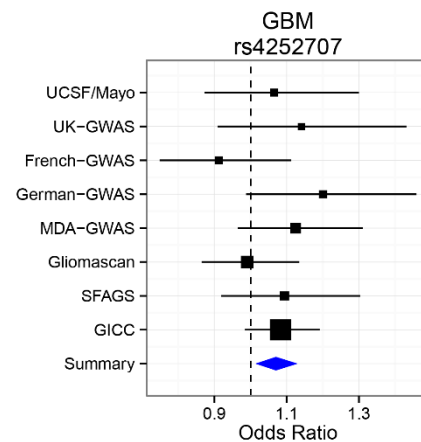
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.867
UK-GWAS	0.881
French-GWAS	0.868
German-GWAS	0.854
MDA-GWAS	0.877
Gliomascan	0.869
SFAGS	0.868
GICC	0.864



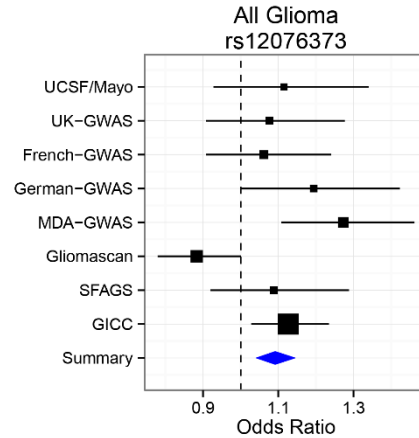
rs4252707 (1q32.1)



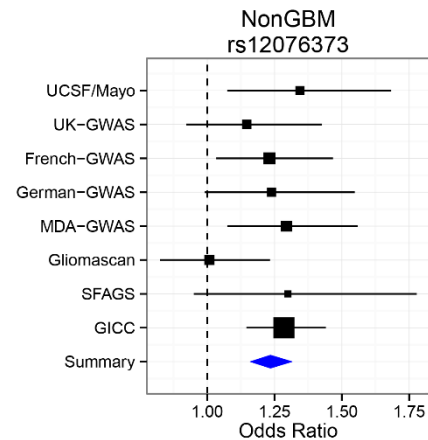
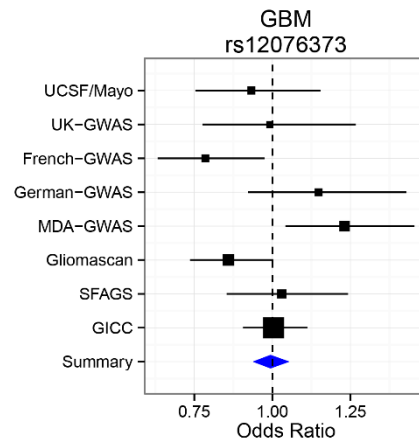
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.203
UK-GWAS	0.184
French-GWAS	0.191
German-GWAS	0.198
MDA-GWAS	0.200
Gliomascan	0.199
SFAGS	0.186
GICC	0.183



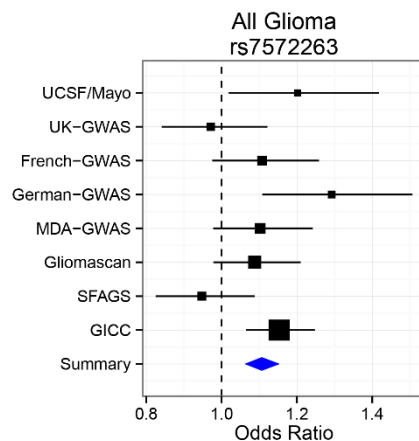
rs12076373 (1q44)



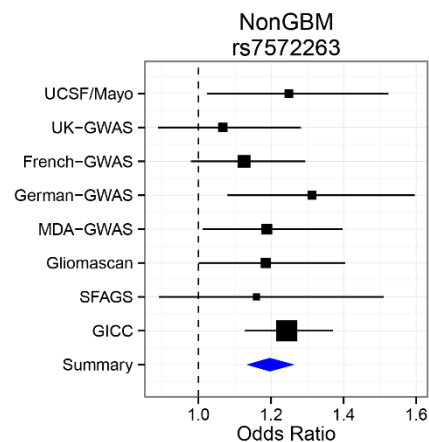
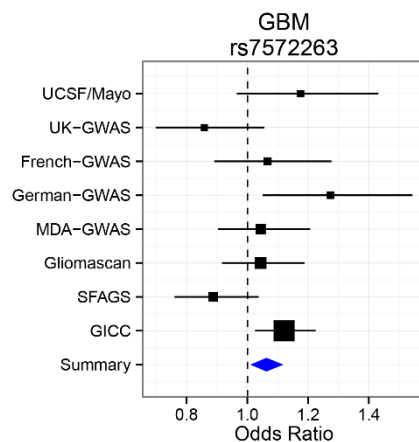
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.833
UK-GWAS	0.851
French-GWAS	0.852
German-GWAS	0.836
MDA-GWAS	0.833
Gliomascan	0.856
SFAGS	0.861
GICC	0.837



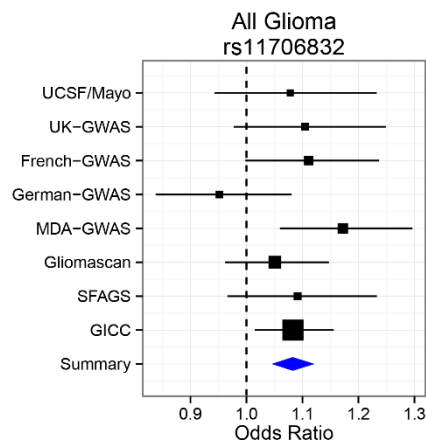
rs7572263 (2q33.3)



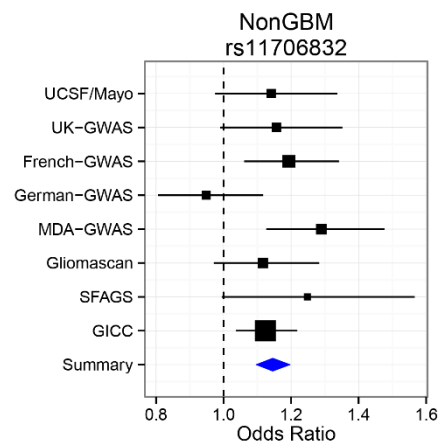
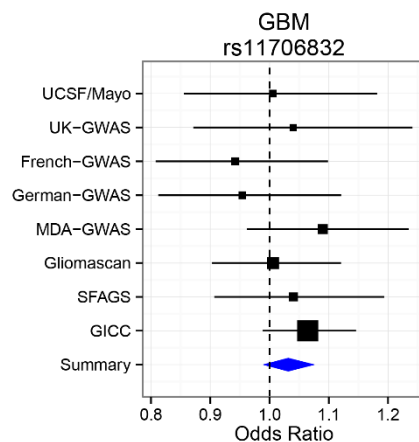
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.765
UK-GWAS	0.767
French-GWAS	0.748
German-GWAS	0.760
MDA-GWAS	0.765
Gliomascan	0.768
SFAGS	0.766
GICC	0.771



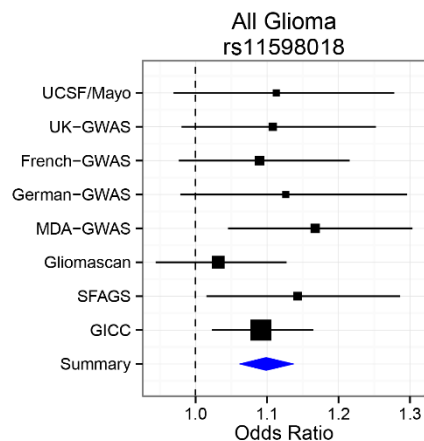
rs11706832 (3p14.1)



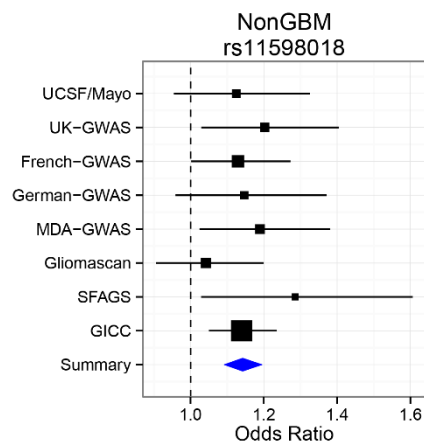
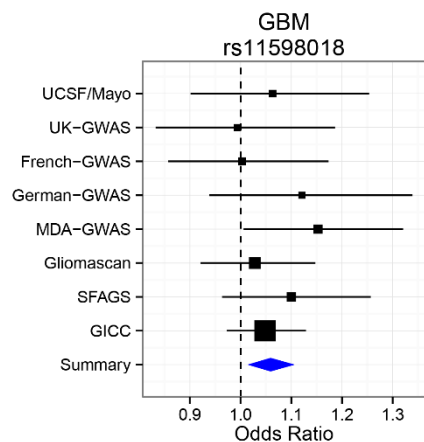
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.465
UK-GWAS	0.474
French-GWAS	0.478
German-GWAS	0.498
MDA-GWAS	0.467
Gliomascan	0.473
SFAGS	0.493
GICC	0.476



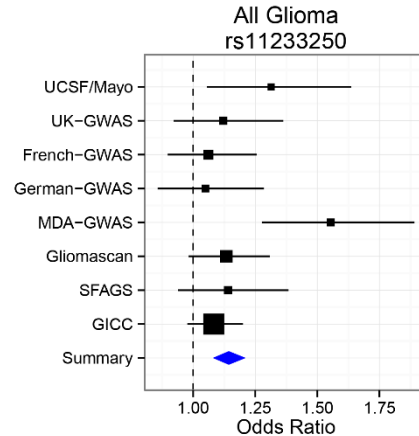
rs11598018 (10q24.33)



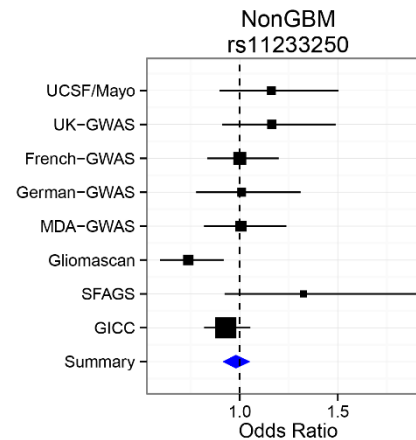
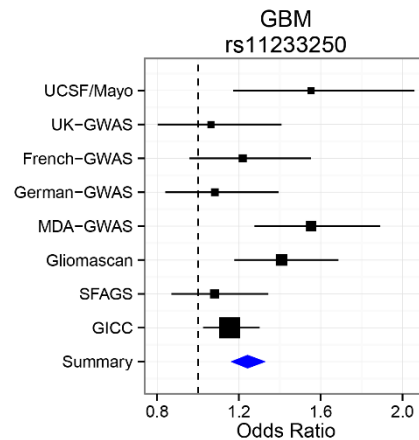
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.505
UK-GWAS	0.506
French-GWAS	0.519
German-GWAS	0.504
MDA-GWAS	0.528
Gliomascan	0.508
SFAGS	0.507
GICC	0.501



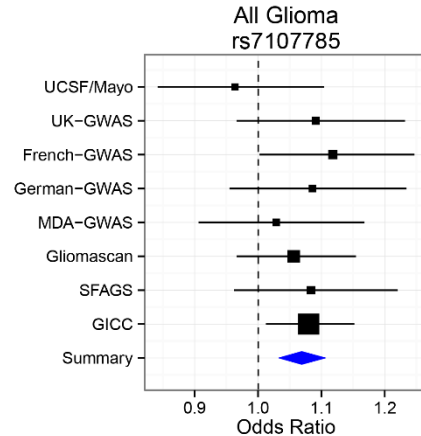
rs11233250 (11q14.1)



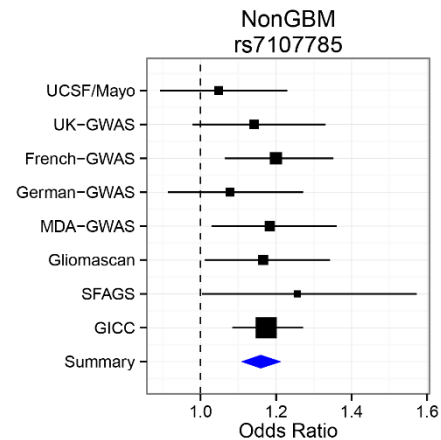
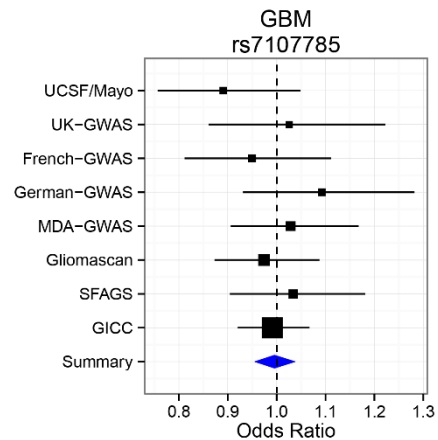
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.879
UK-GWAS	0.887
French-GWAS	0.881
German-GWAS	0.881
MDA-GWAS	0.878
Gliomascan	0.888
SFAGS	0.885
GICC	0.881



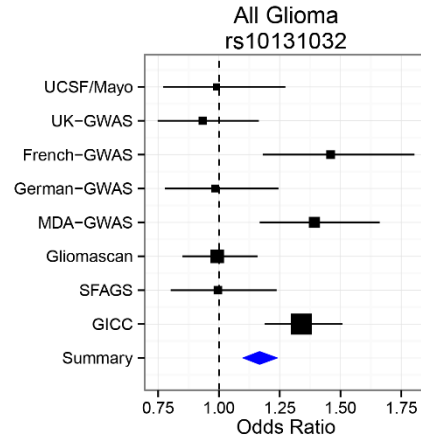
rs7107785 (11q21)



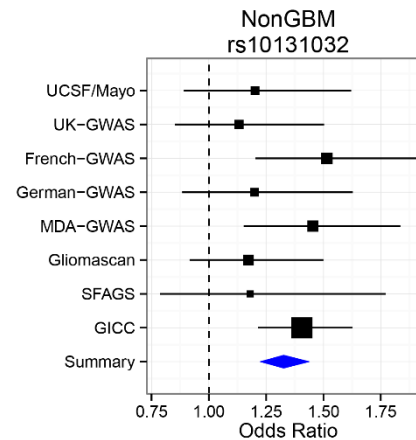
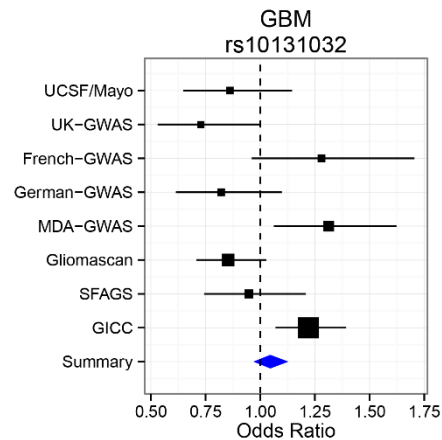
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.501
UK-GWAS	0.511
French-GWAS	0.520
German-GWAS	0.513
MDA-GWAS	0.510
Gliomascan	0.519
SFAGS	0.532
GICC	0.511



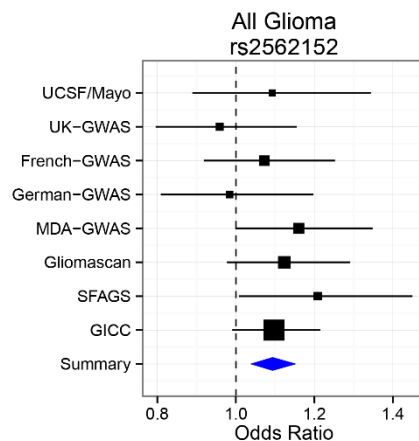
rs10131032 (14q12)



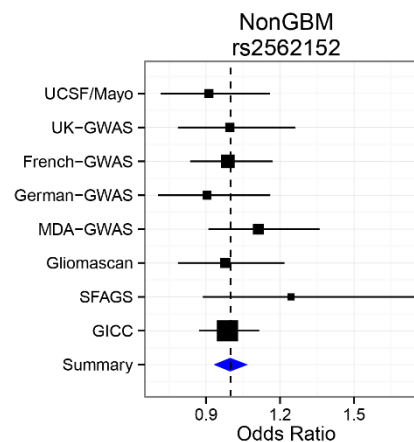
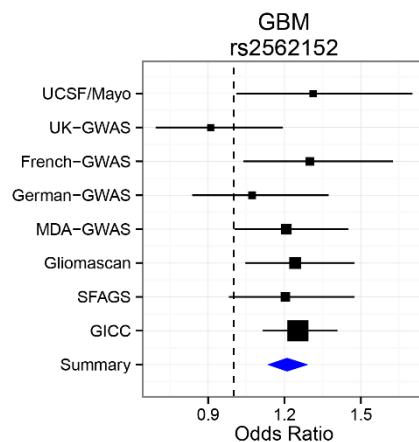
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.914
UK-GWAS	0.917
French-GWAS	0.914
German-GWAS	0.921
MDA-GWAS	0.898
Gliomascan	0.911
SFAGS	0.919
GICC	0.902



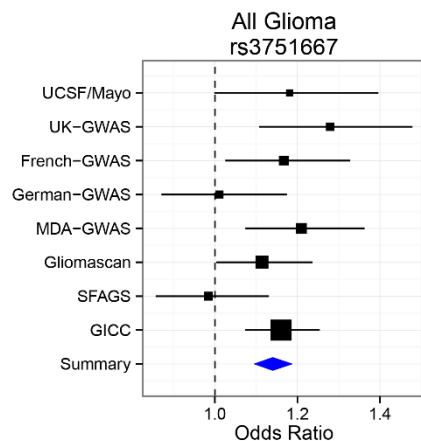
rs2562152 (16p13.3)



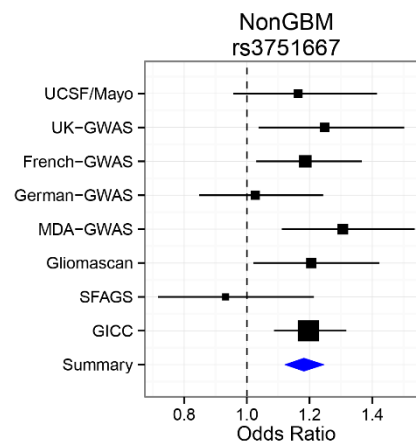
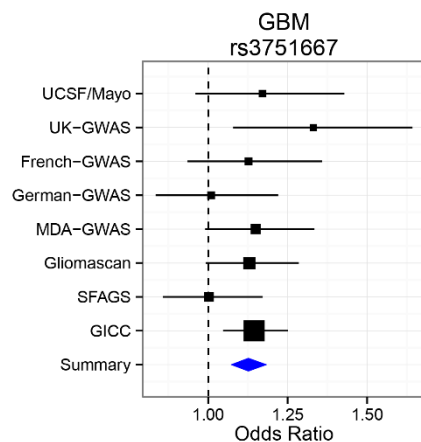
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.128
UK-GWAS	0.133
French-GWAS	0.153
German-GWAS	0.133
MDA-GWAS	0.143
Gliomascan	0.130
SFAGS	0.141
GICC	0.134



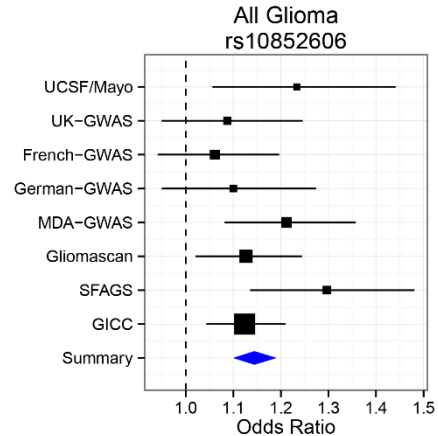
rs3751667 (16p13.3)



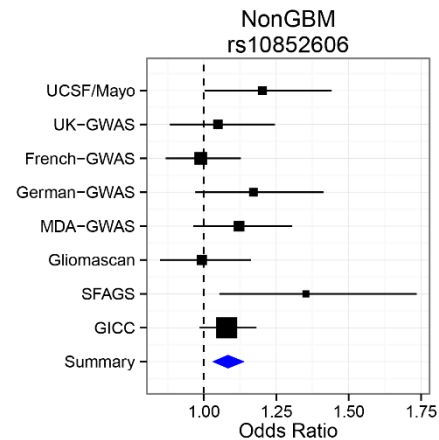
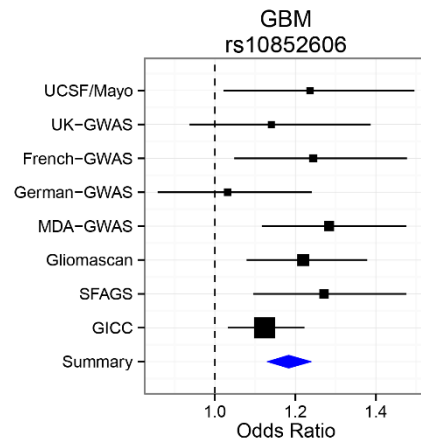
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.221
UK-GWAS	0.225
French-GWAS	0.206
German-GWAS	0.238
MDA-GWAS	0.232
Gliomascan	0.228
SFAGS	0.242
GICC	0.235



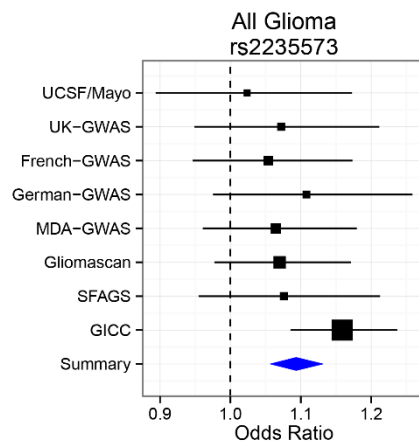
rs10852606 (16q12.1)



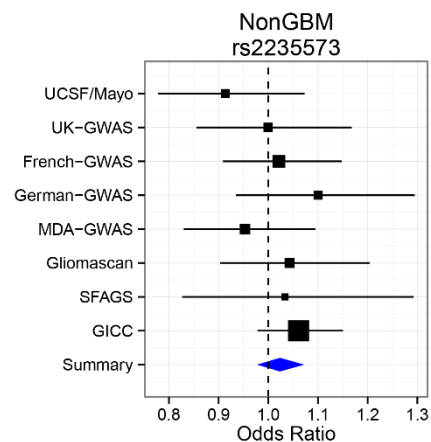
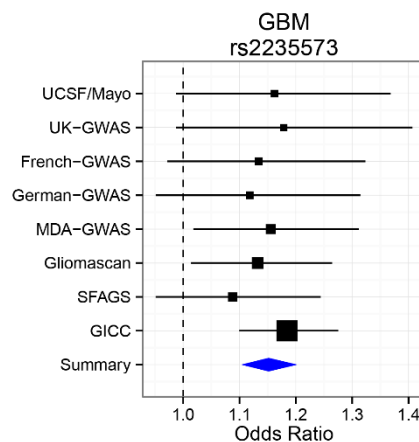
STUDY	MAF (CONTROLS)
UCSF/Mayo	0.291
UK-GWAS	0.288
French-GWAS	0.299
German-GWAS	0.260
MDA-GWAS	0.291
Gliomascan	0.283
SFAGS	0.297
GICC	0.281



rs2235573 (22q13.1)



STUDY	MAF (CONTROLS)
UCSF/Mayo	0.503
UK-GWAS	0.513
French-GWAS	0.538
German-GWAS	0.513
MDA-GWAS	0.509
Gliomascan	0.507
SFAGS	0.519
GICC	0.492

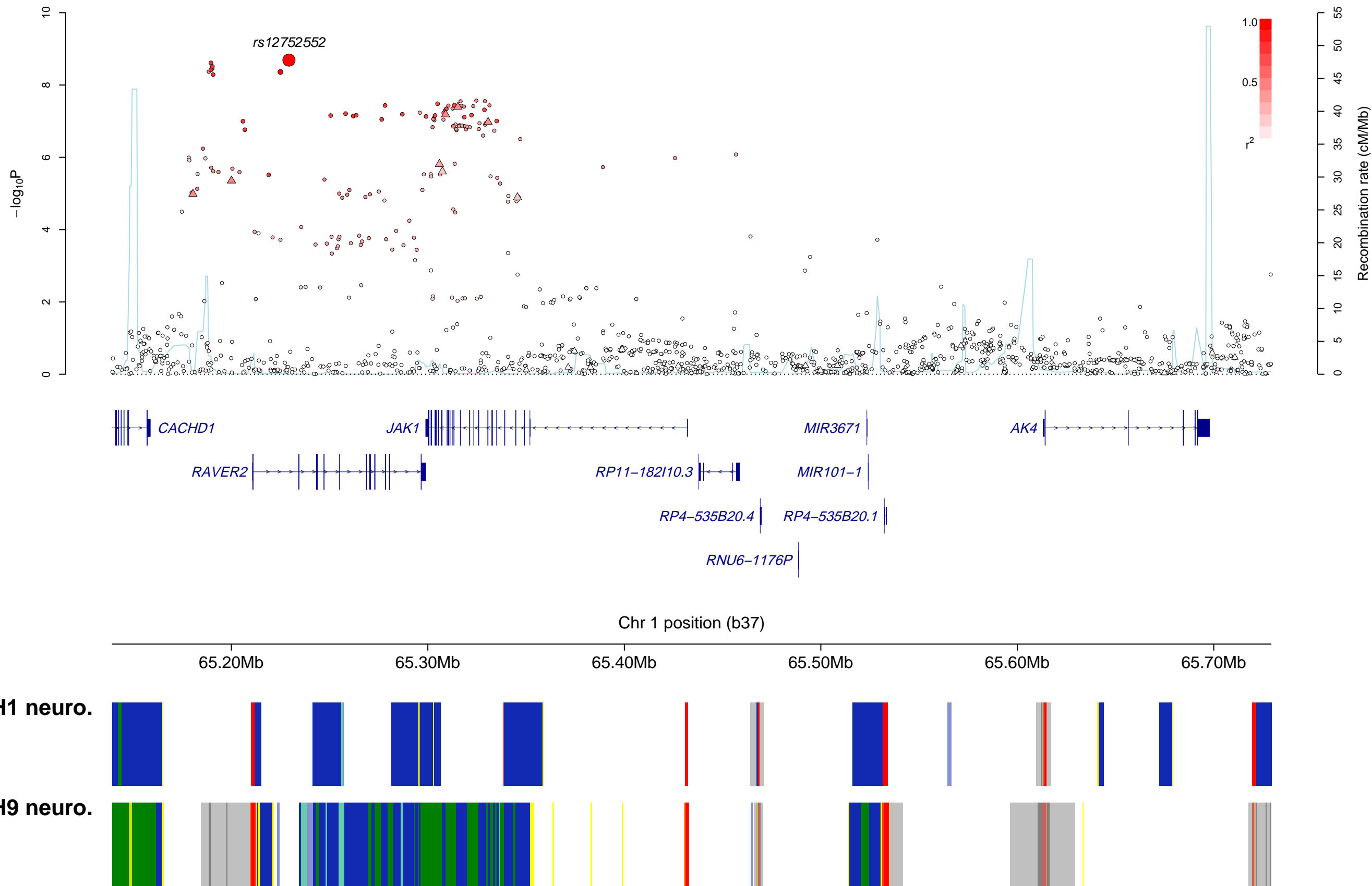


Supplementary Figure 3: Regional plots of discovery-phase association results, recombination rates and chromatin state segmentation tracks for the new glioma risk loci.

Plots show discovery association results of both genotyped (triangles) and imputed (circles) SNPs in the GWAS samples and recombination rates. $-\log_{10} P$ values (y axes) of the SNPs are shown according to their chromosomal positions (x axes). The lead SNP in each combined analysis is shown as a large circle or triangle (if imputed or directly genotyped respectively) and is labeled by its rsID. The color intensity of each symbol reflects the extent of LD with the top genotyped SNP, white ($r^2 = 0$) through to dark red ($r^2 = 1.0$). Genetic recombination rates, estimated using HapMap samples from Utah residents of western and northern European ancestry (CEU), are shown with a light blue line. Physical positions are based on NCBI build 37 of the human genome. Also shown are the relative positions of GENCODE v19 genes mapping to the region of association. Below each plot is a diagram of the exons and introns of the genes of interest, the associated SNPs and the chromatin state segmentation track (ChromHMM) for H1 and H9 neural progenitor cells derived from the epigenome roadmap project, as per the chromHMM legend at the end of the figure. TSS, transcriptional start sites.

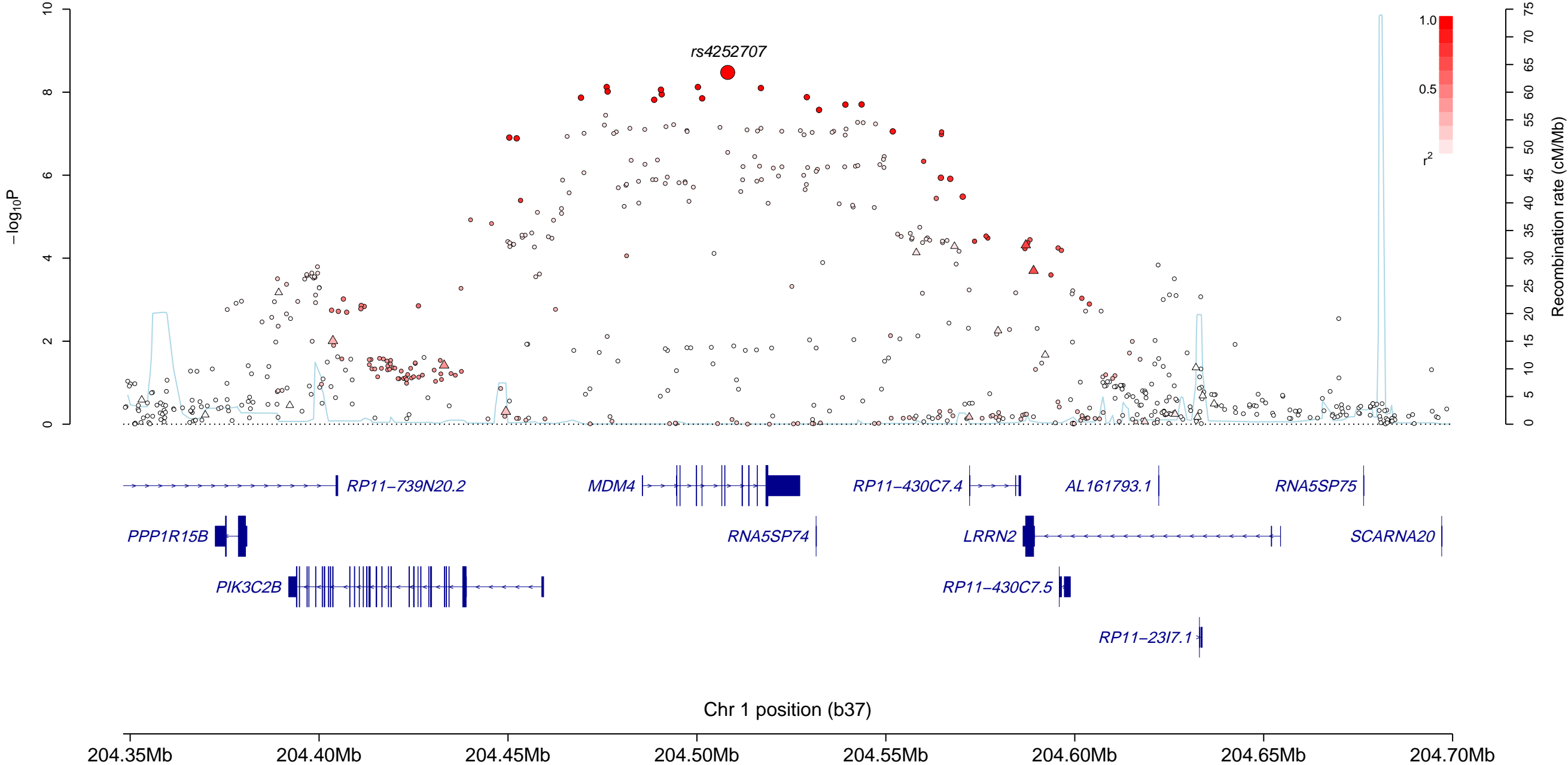
a)

1p31.3 (GBM)

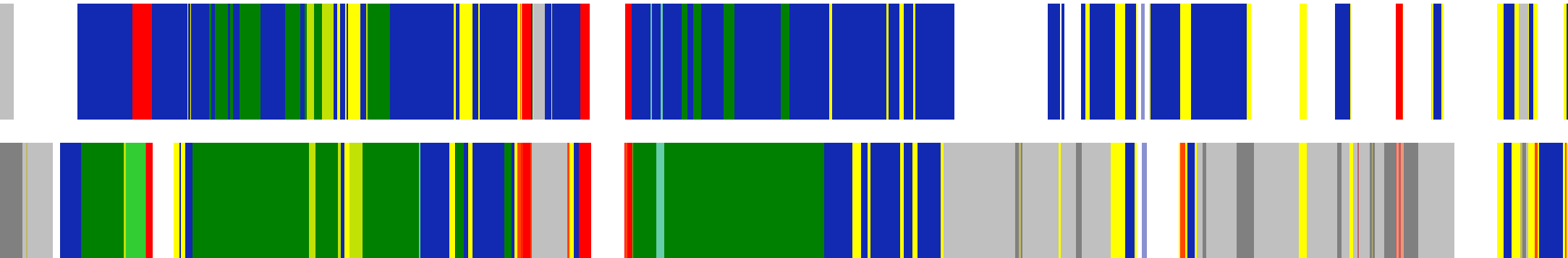


b)

1q32.1 (non-GBM)



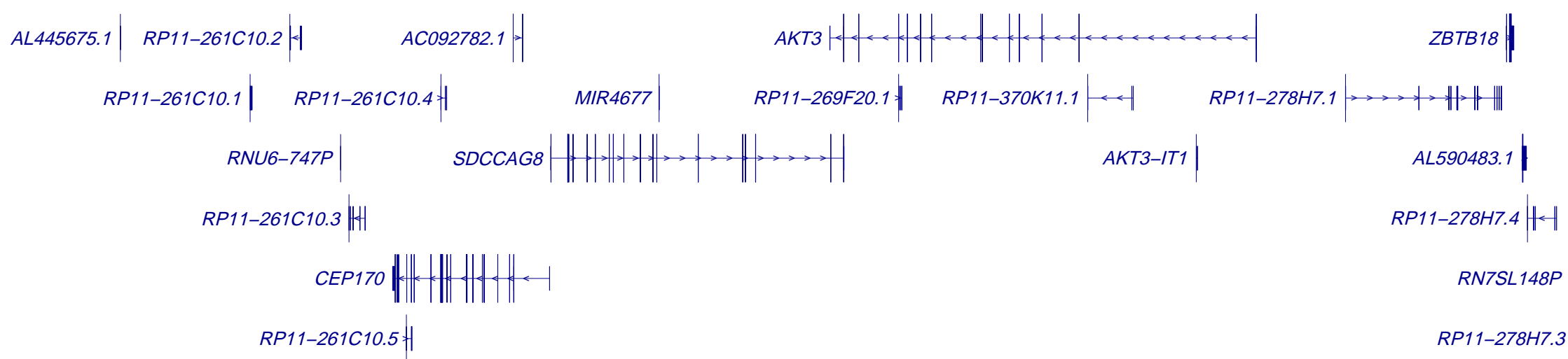
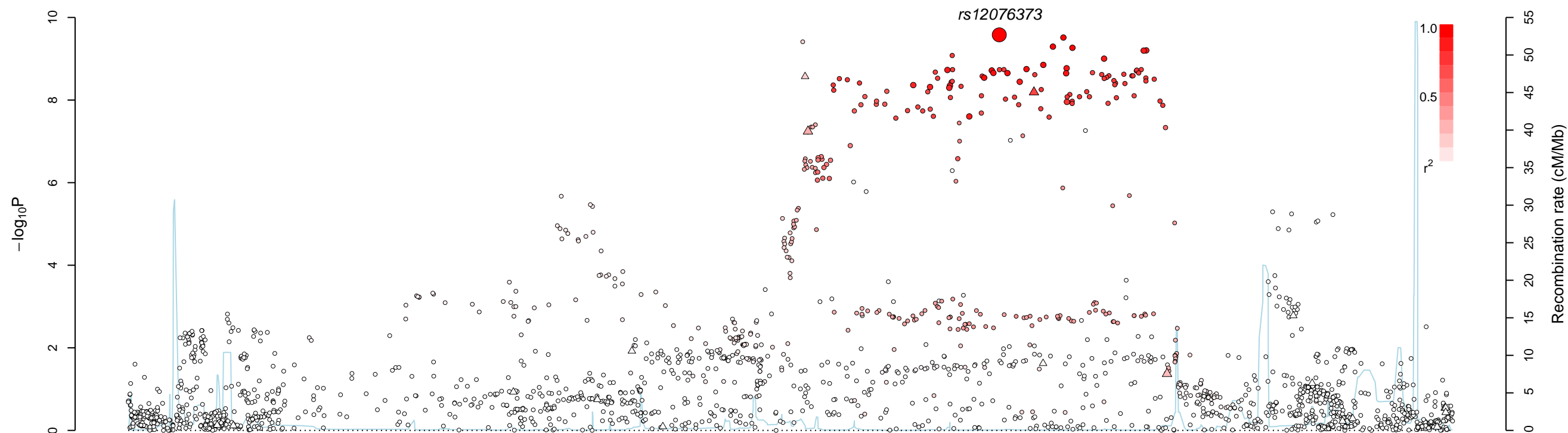
H1 neuro



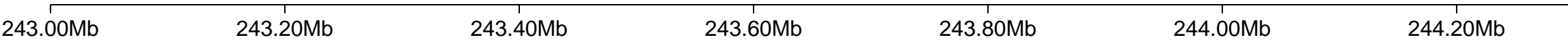
H9 neuro

c)

1q44 (non-GBM)

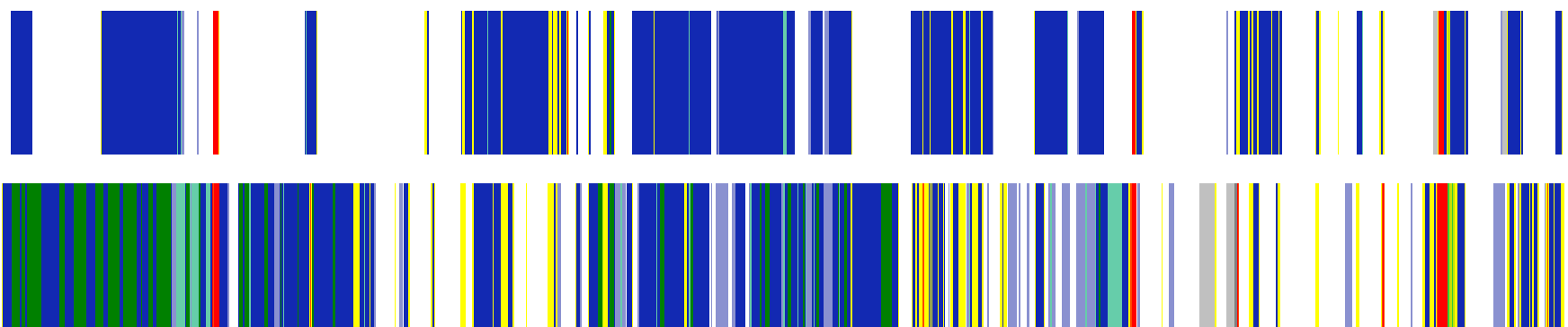


Chr 1 position (b37)



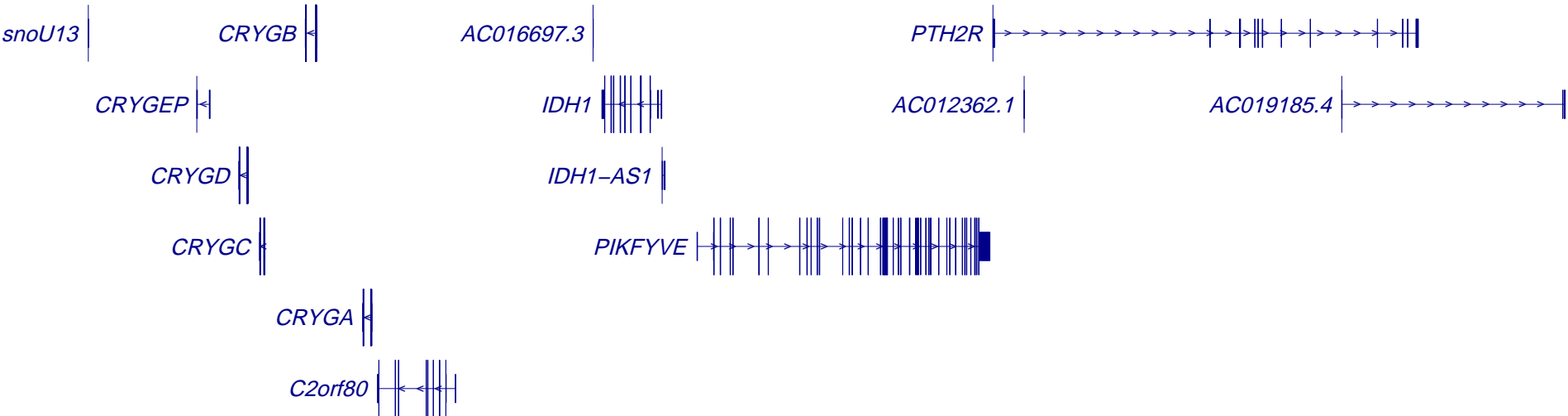
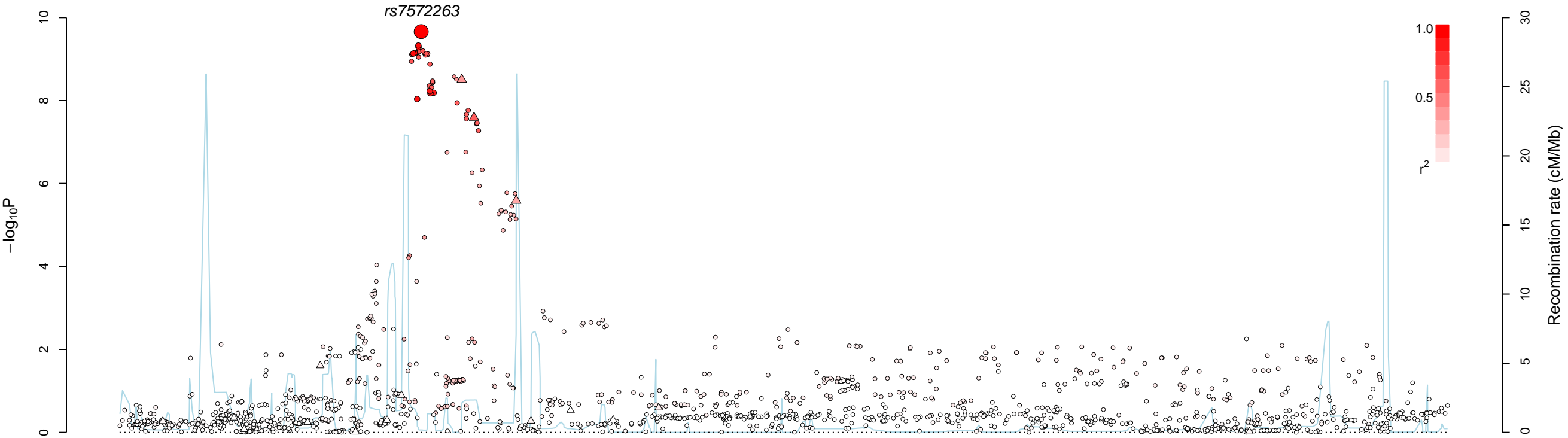
H1 neuro.

H9 neuro.



d)

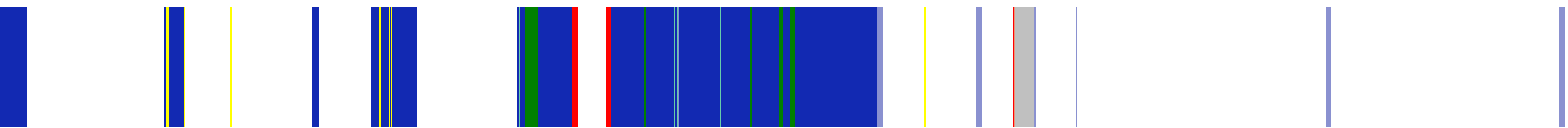
2q33.3 (non-GBM)



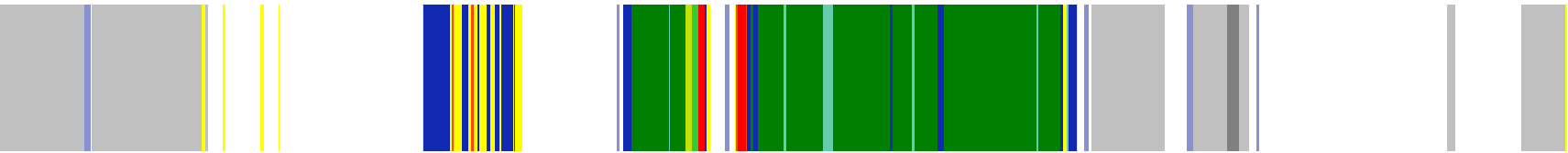
Chr 2 position (b37)

208.90Mb 209.00Mb 209.10Mb 209.20Mb 209.30Mb 209.40Mb 209.50Mb

H1 neuro.

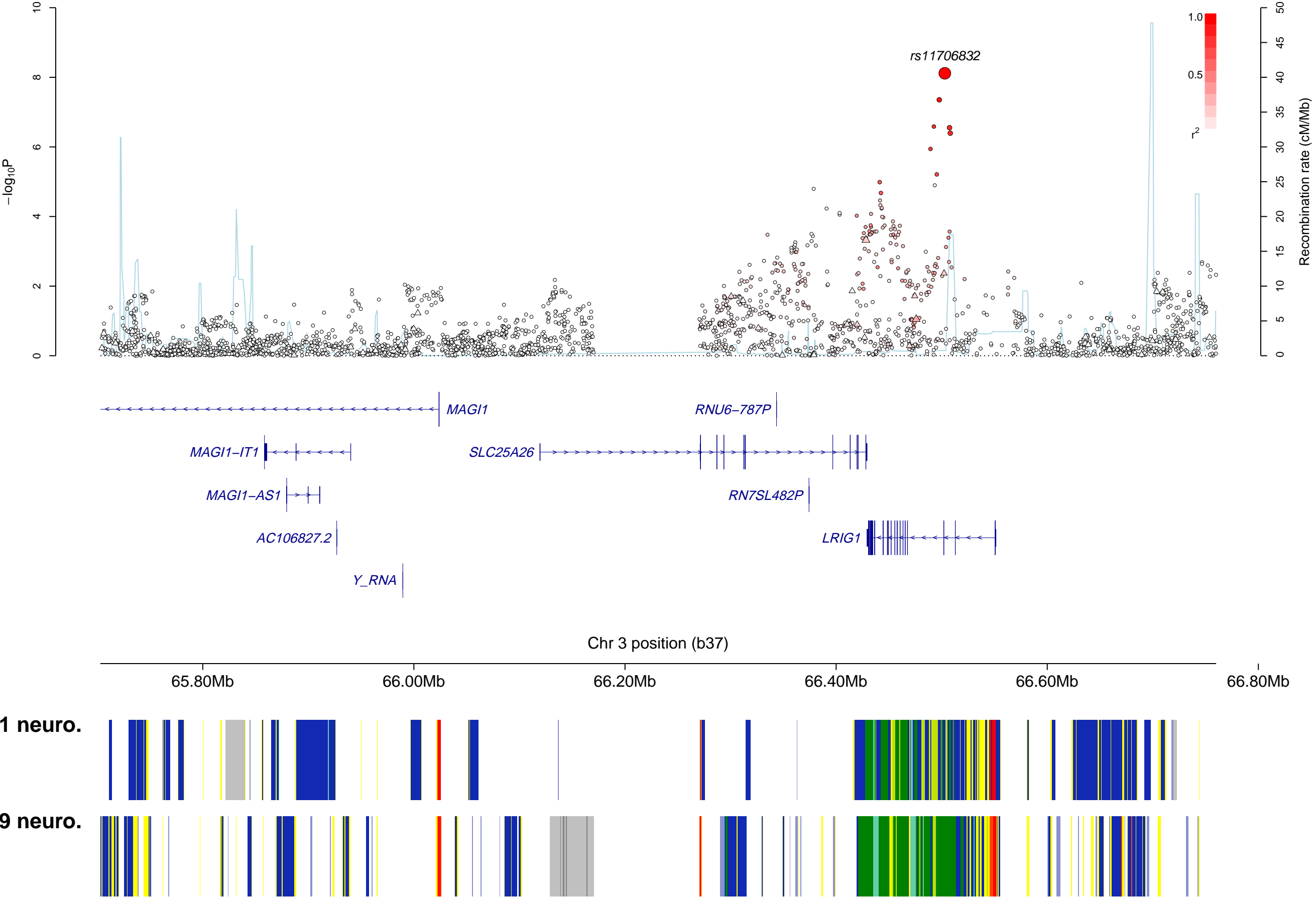


H9 neuro.

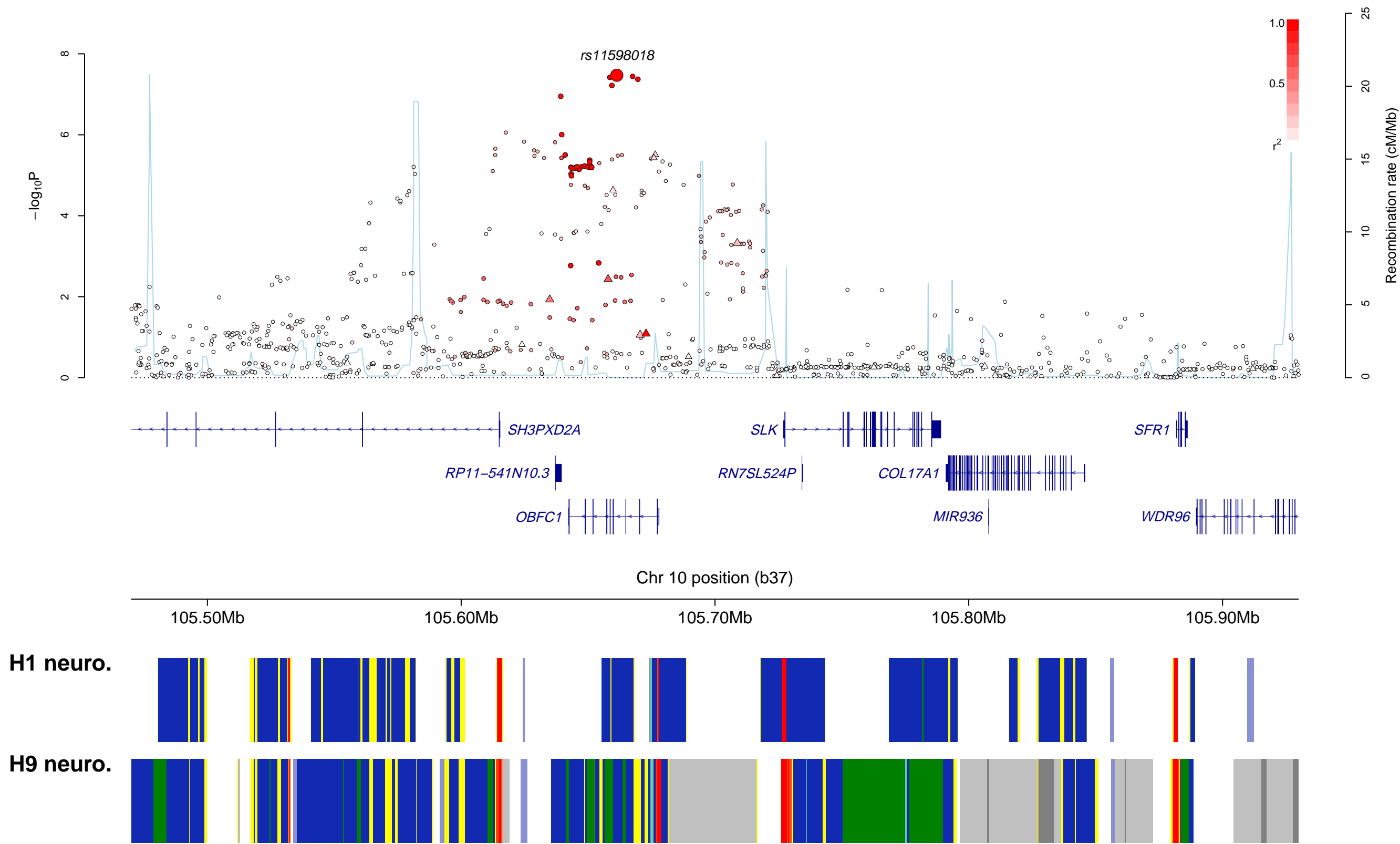


e)

3p14.1 (non-GBM)

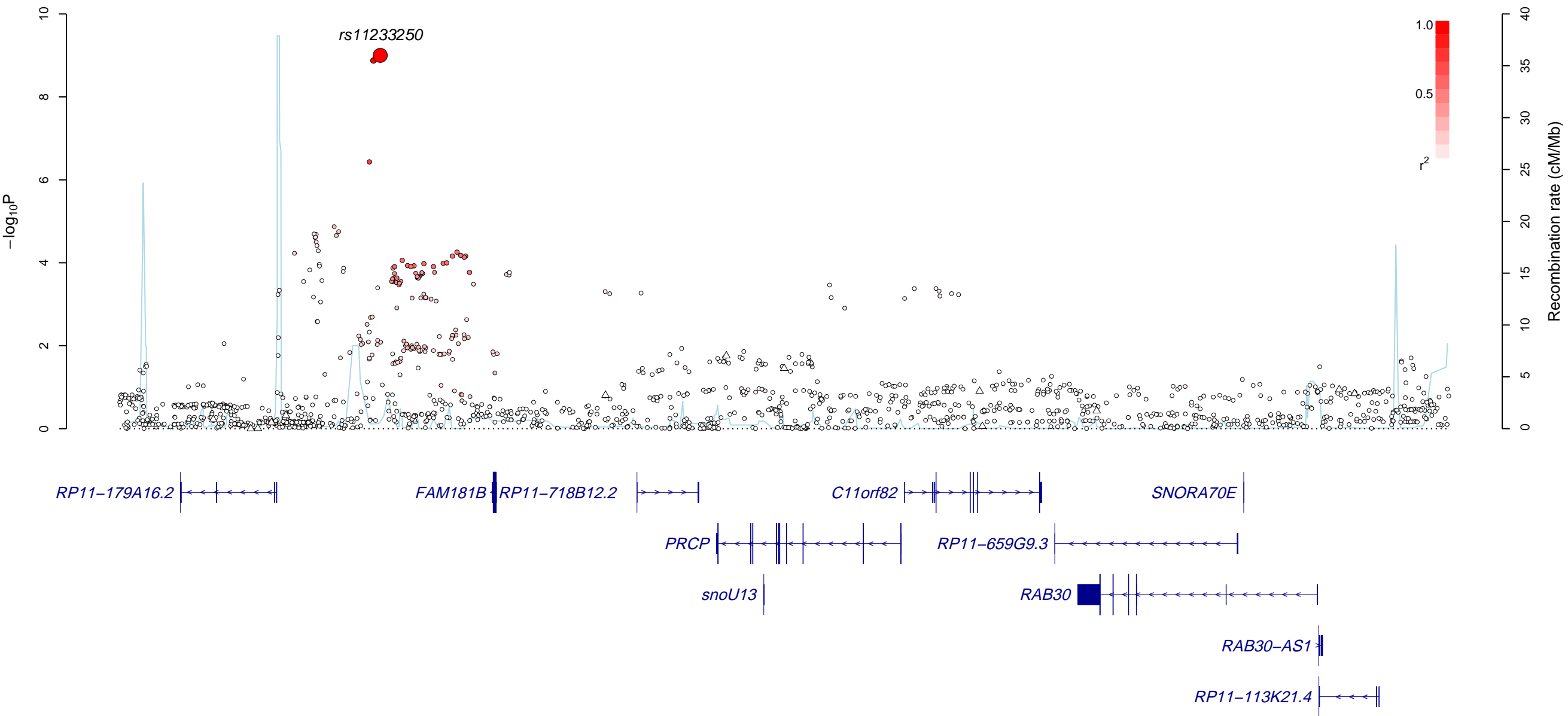


f) 10q24.33 (non-GBM)



g)

11q14.1 (GBM)

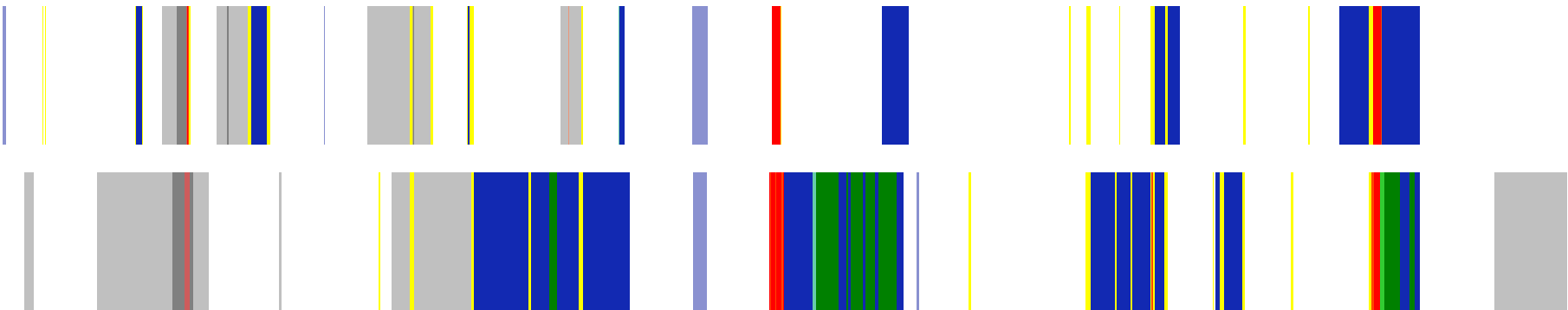


Chr 11 position (b37)

82.30Mb 82.40Mb 82.50Mb 82.60Mb 82.70Mb 82.80Mb

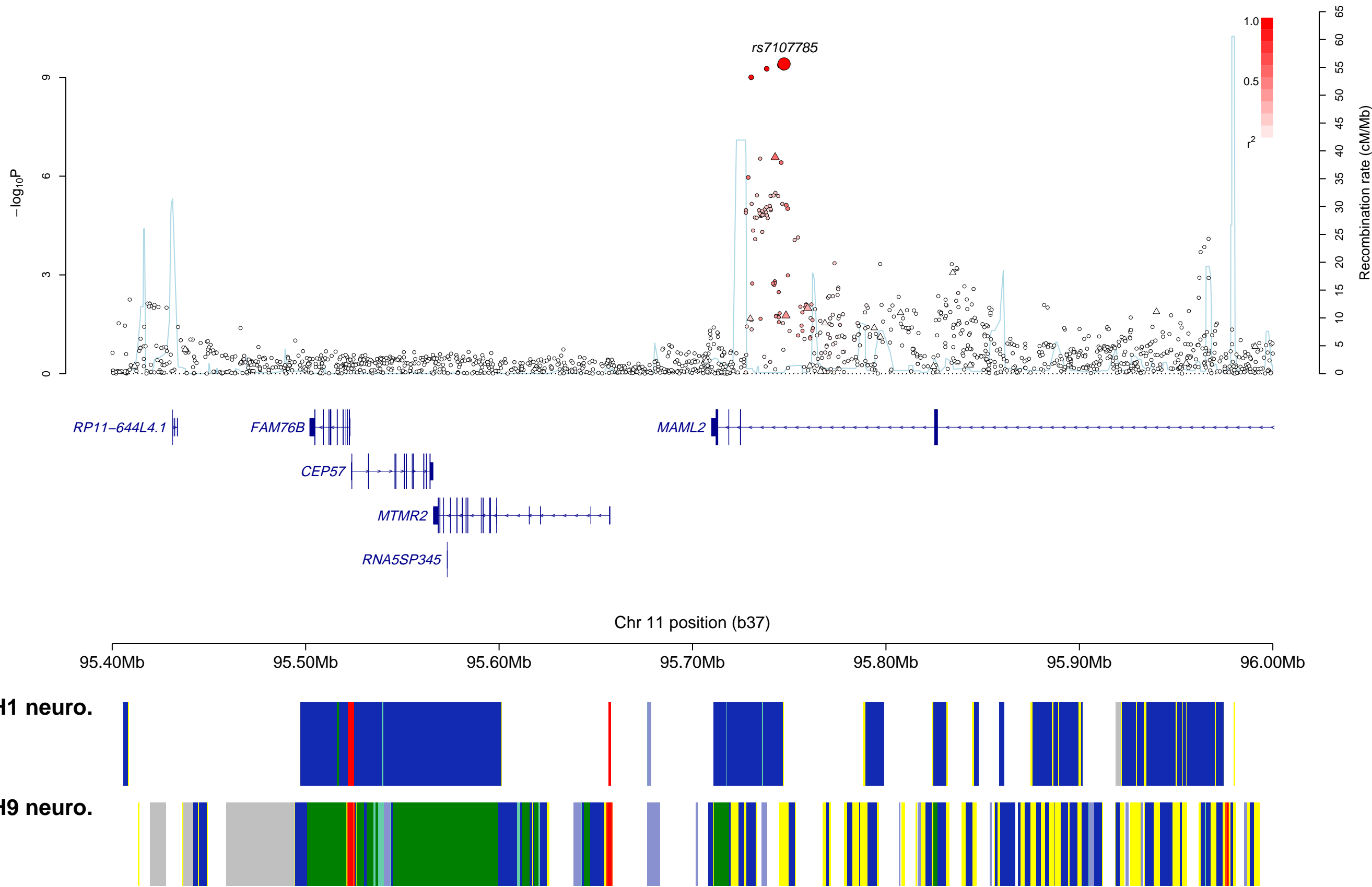
H1 neuro.

H9 neuro.



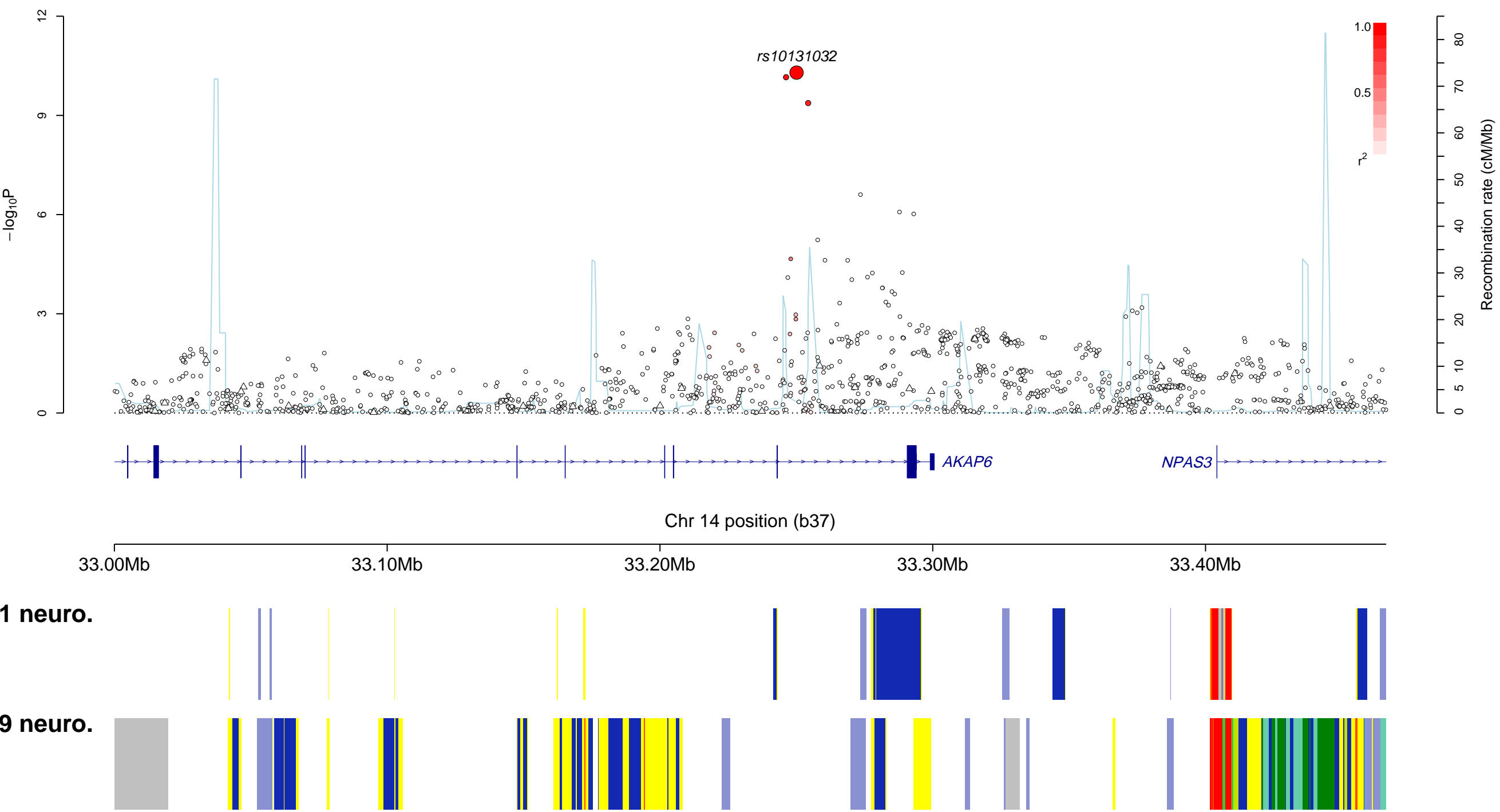
h)

11q21 (non-GBM)



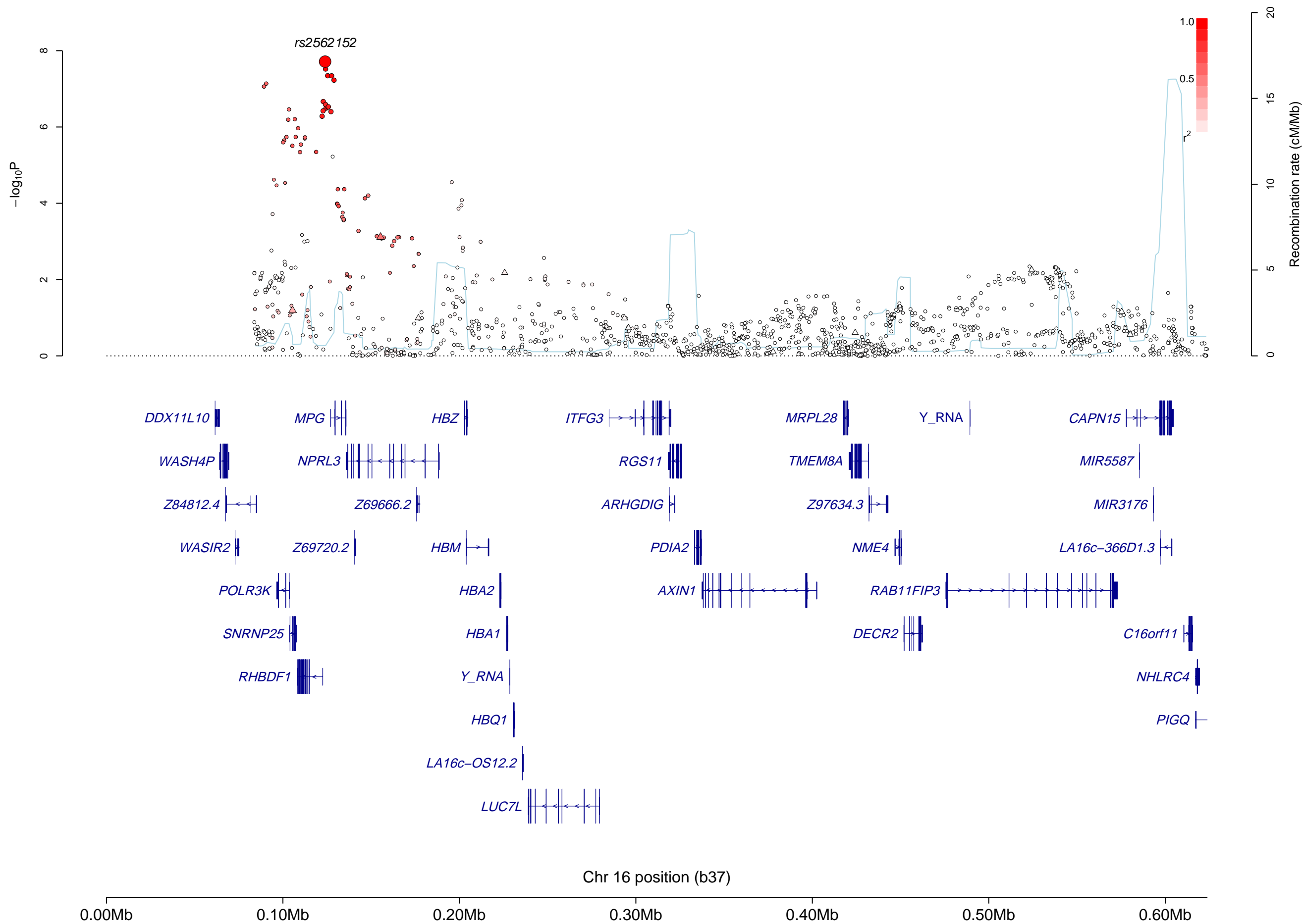
i)

14q12 (non-GBM)



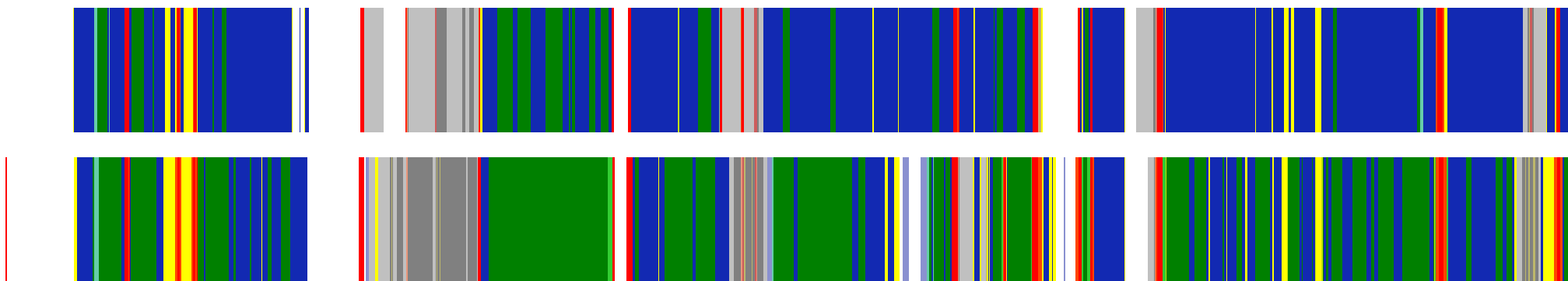
16p13.3 (GBM)

j)



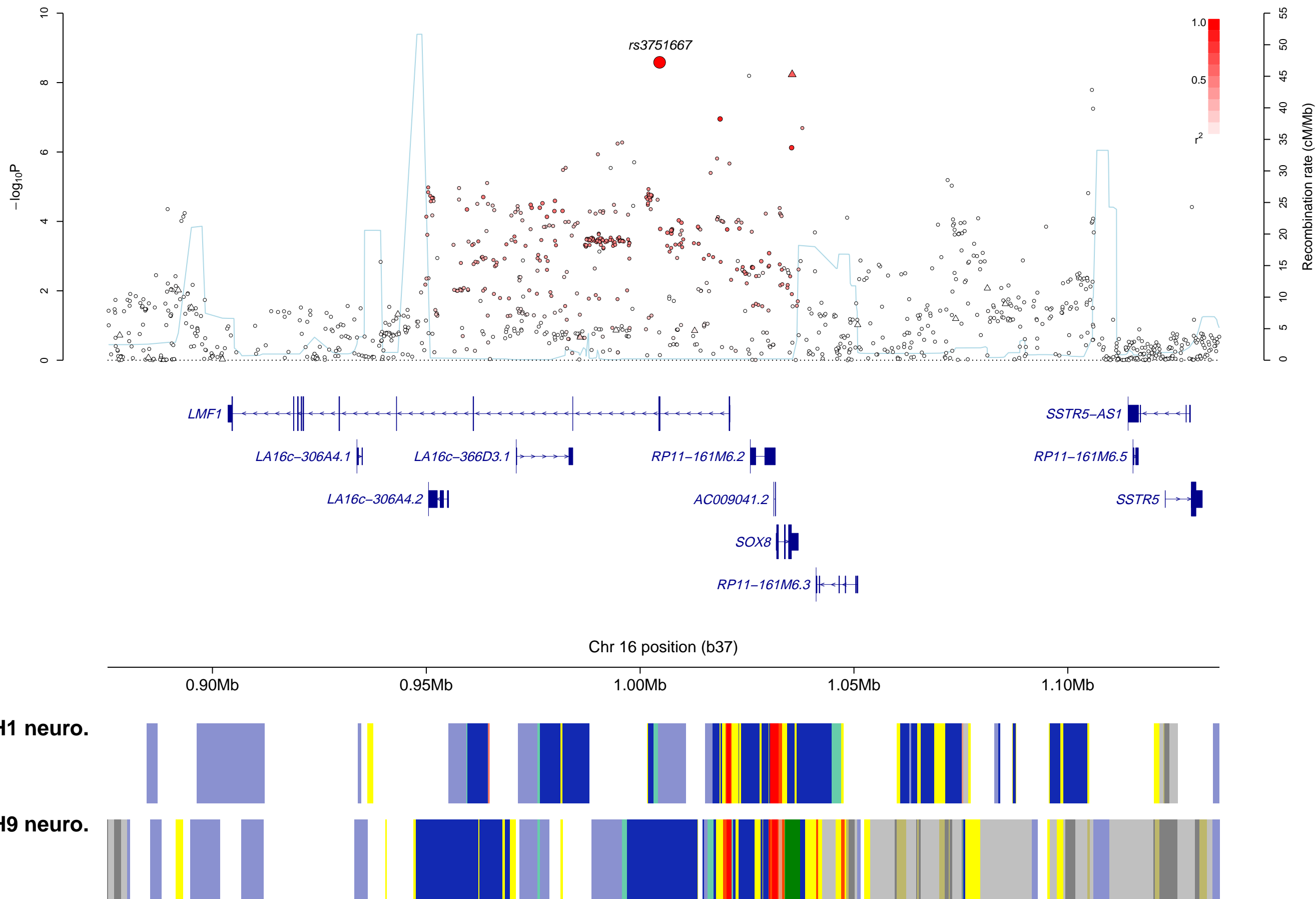
H1 neuro.

H9 neuro.



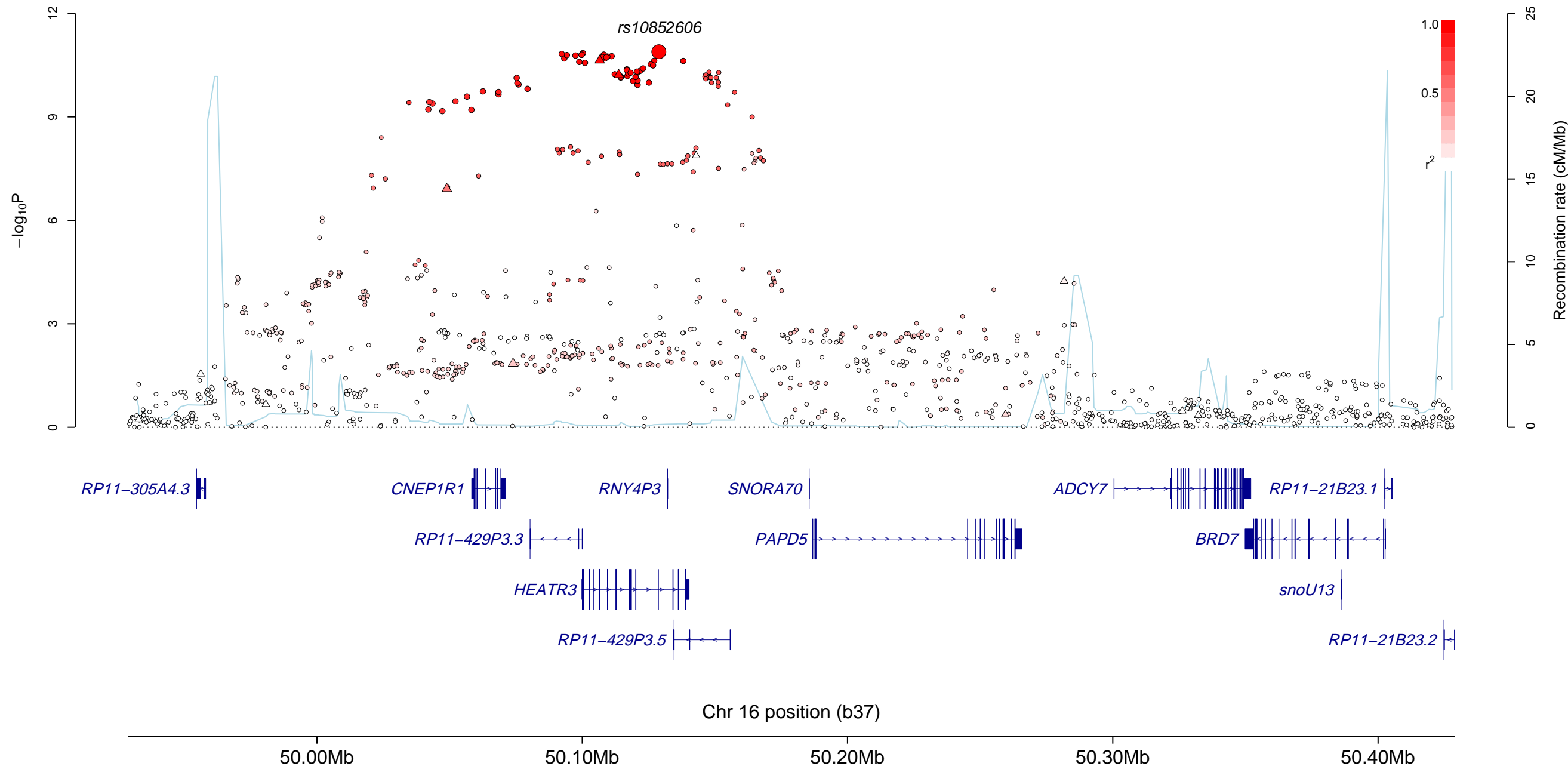
k)

16p13.3 (non-GBM)



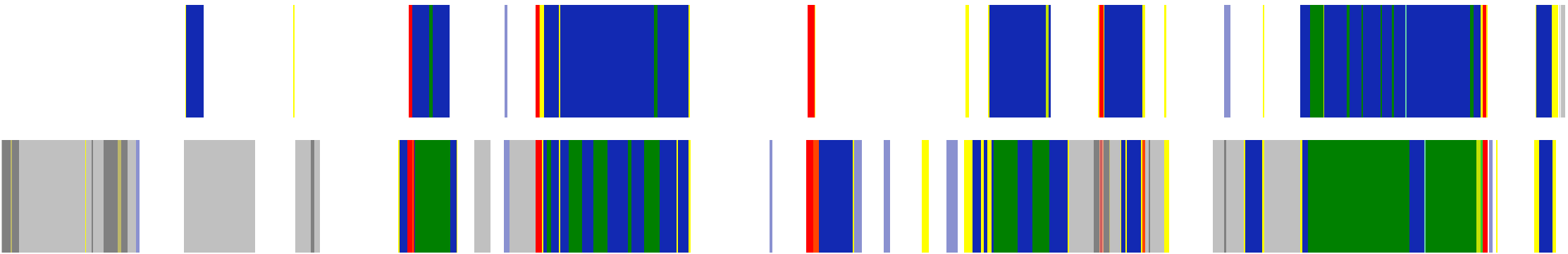
I)

16q12.1 (GBM)

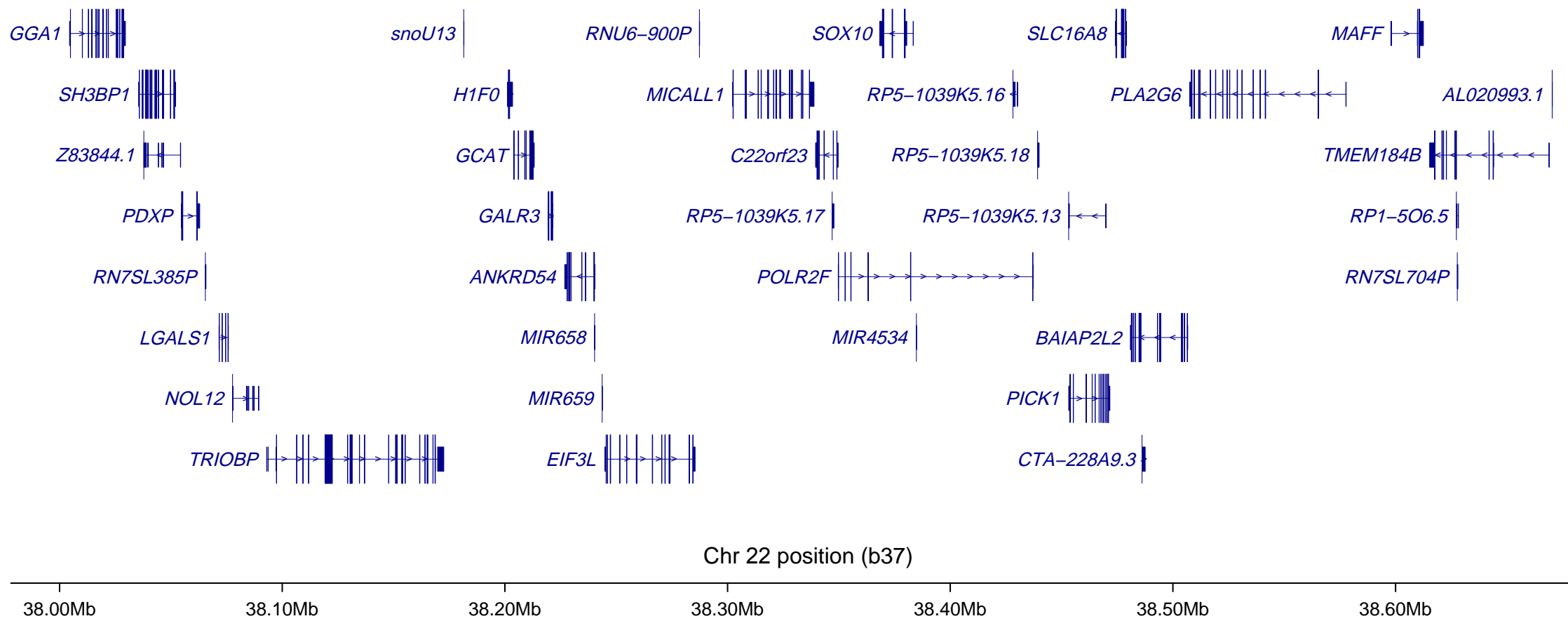
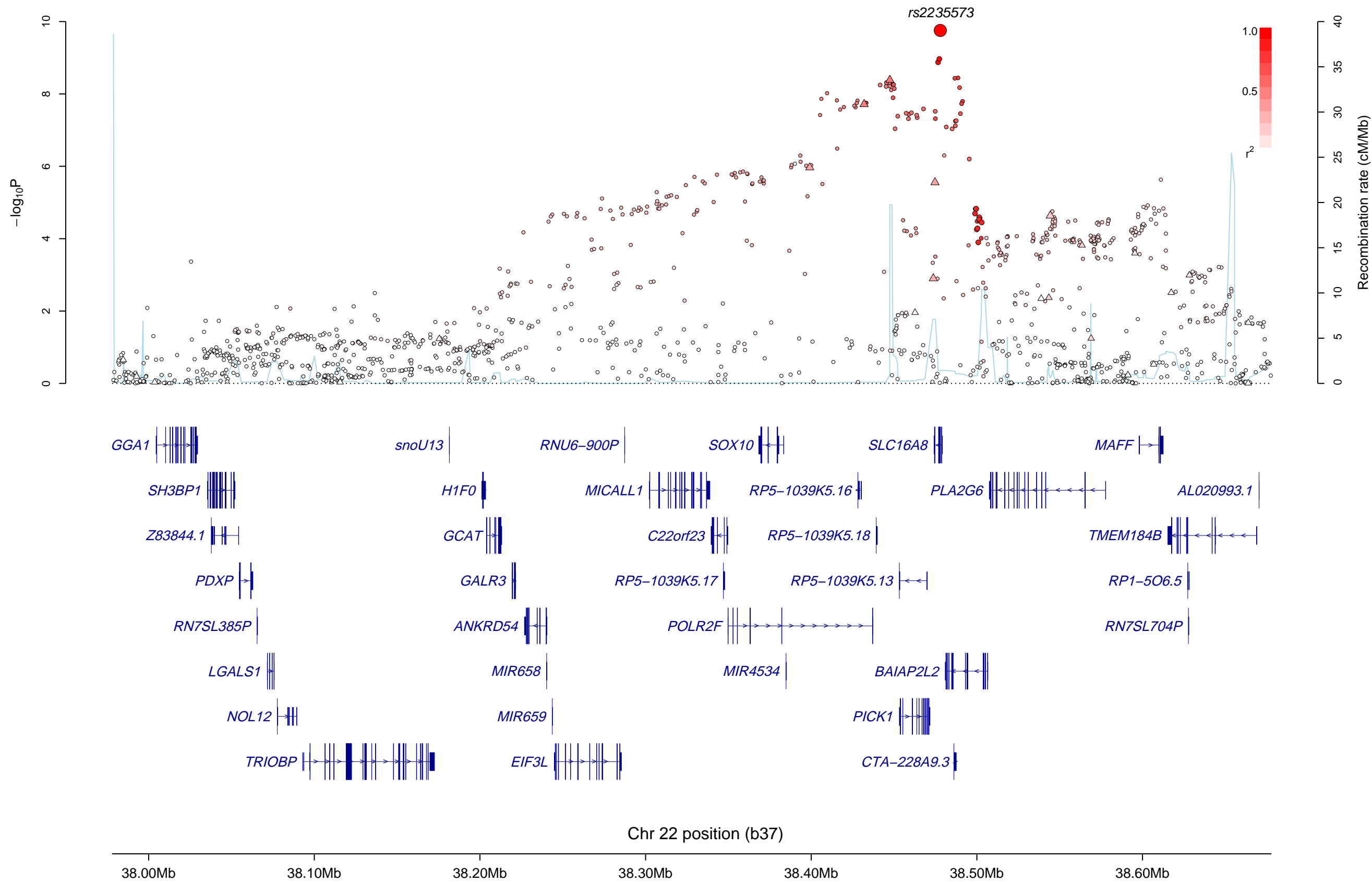


H1 neuro.

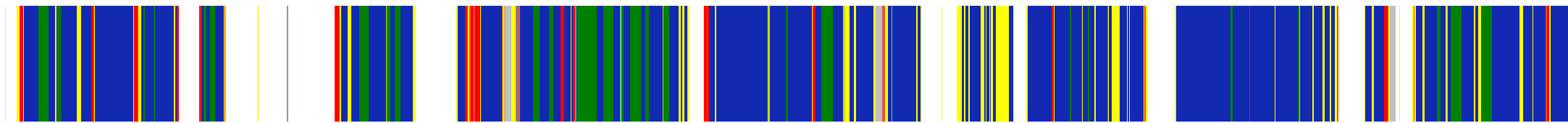
H9 neuro.



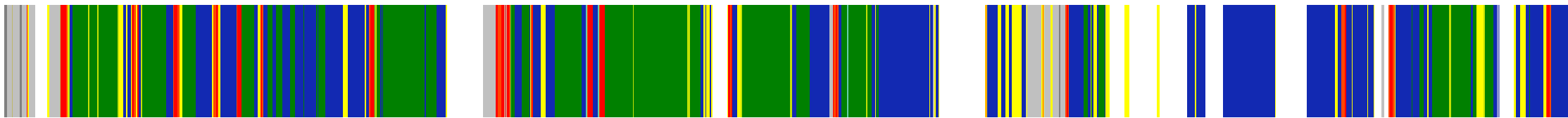
m) 22q13.1 (GBM)


















H1 neuro.



H9 neuro.



ChromHMM legend

	Active TSS		Genic enhancers		Flanking bivalent TSS/Enh
	Flanking active TSS		Enhancers		Bivalent enhancer
	Transcr. at gene 5'+3'		ZNF genes + repeats		Repressed Polycomb
	Strong transcription		Heterochromatin		Weak repressed Polycomb
	Weak transcription		Bivalent/poised TSS		Quiescent/low

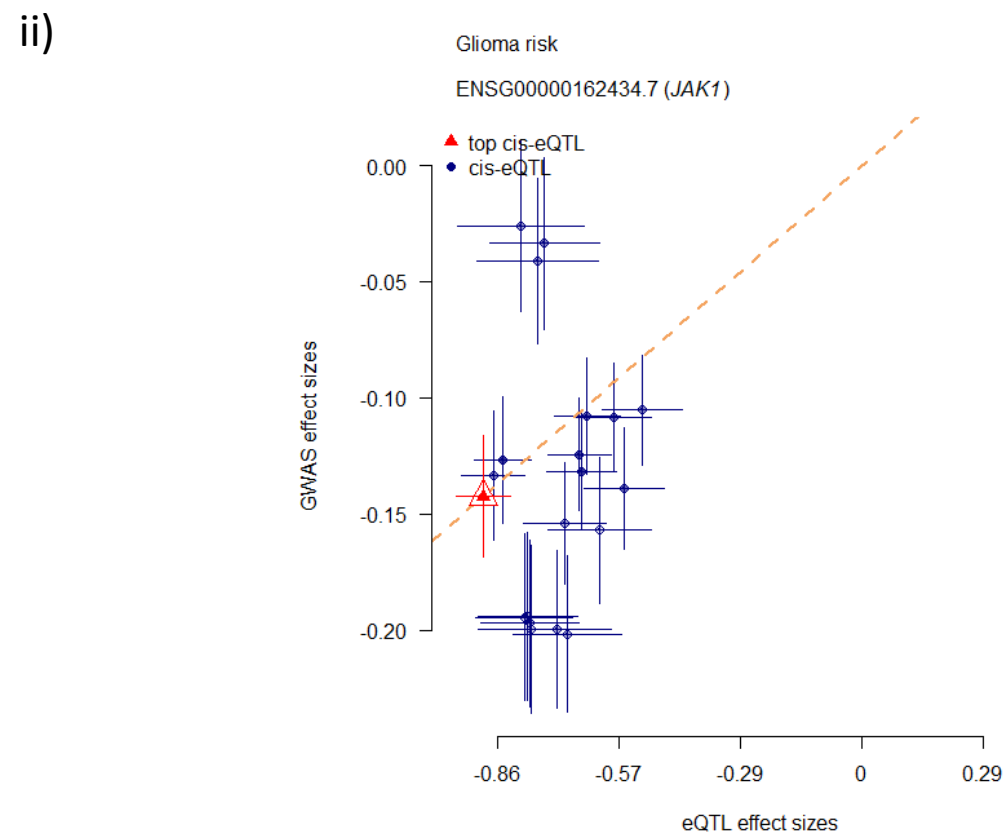
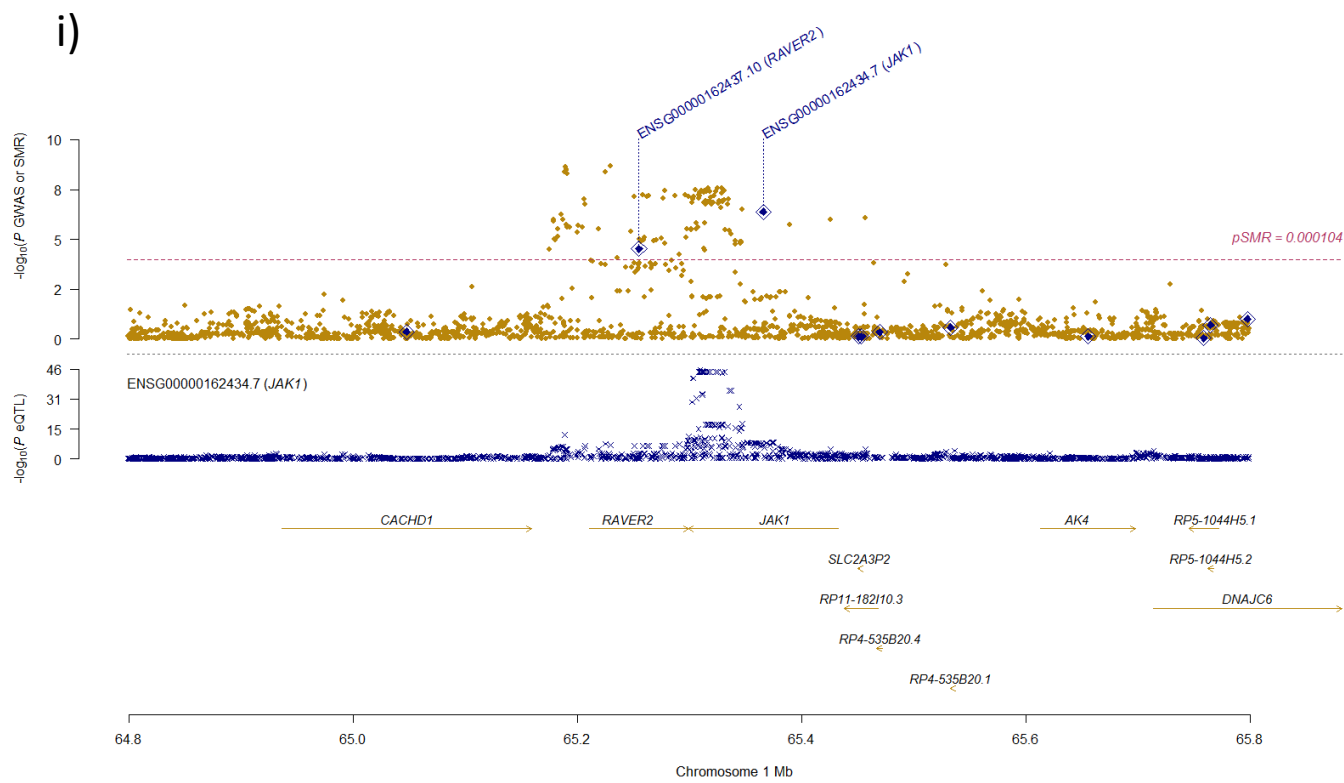
Supplementary Figure 4: SMR eQTL plots

At each locus:

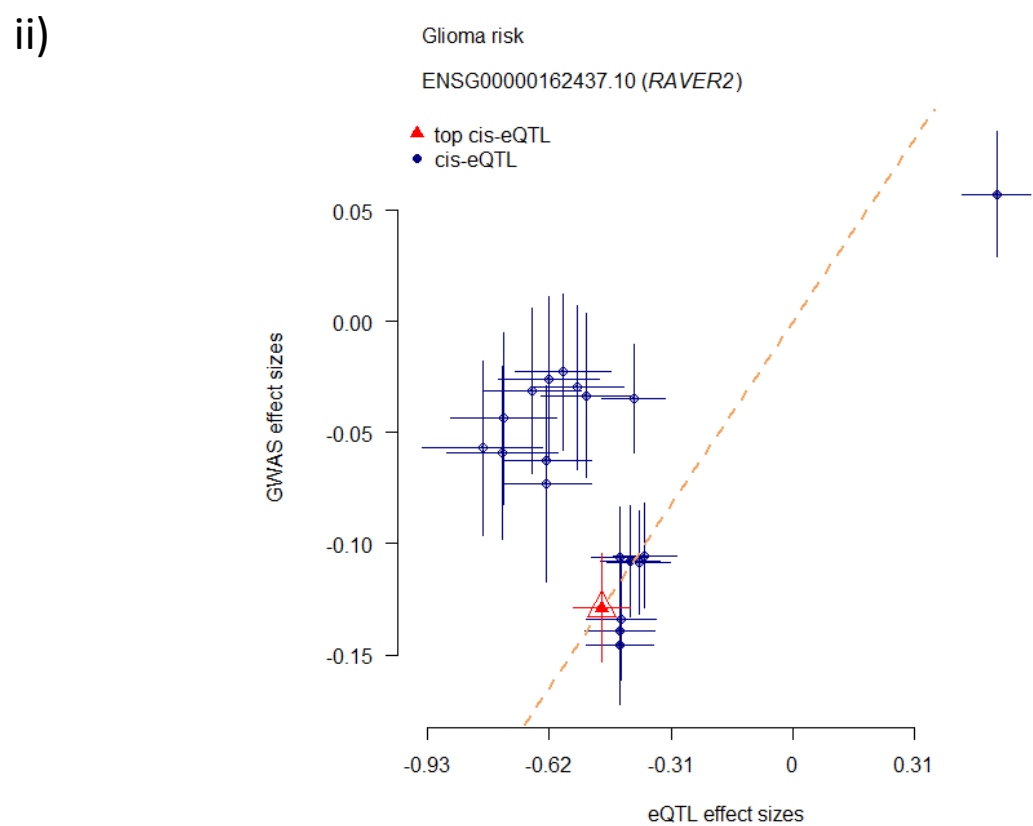
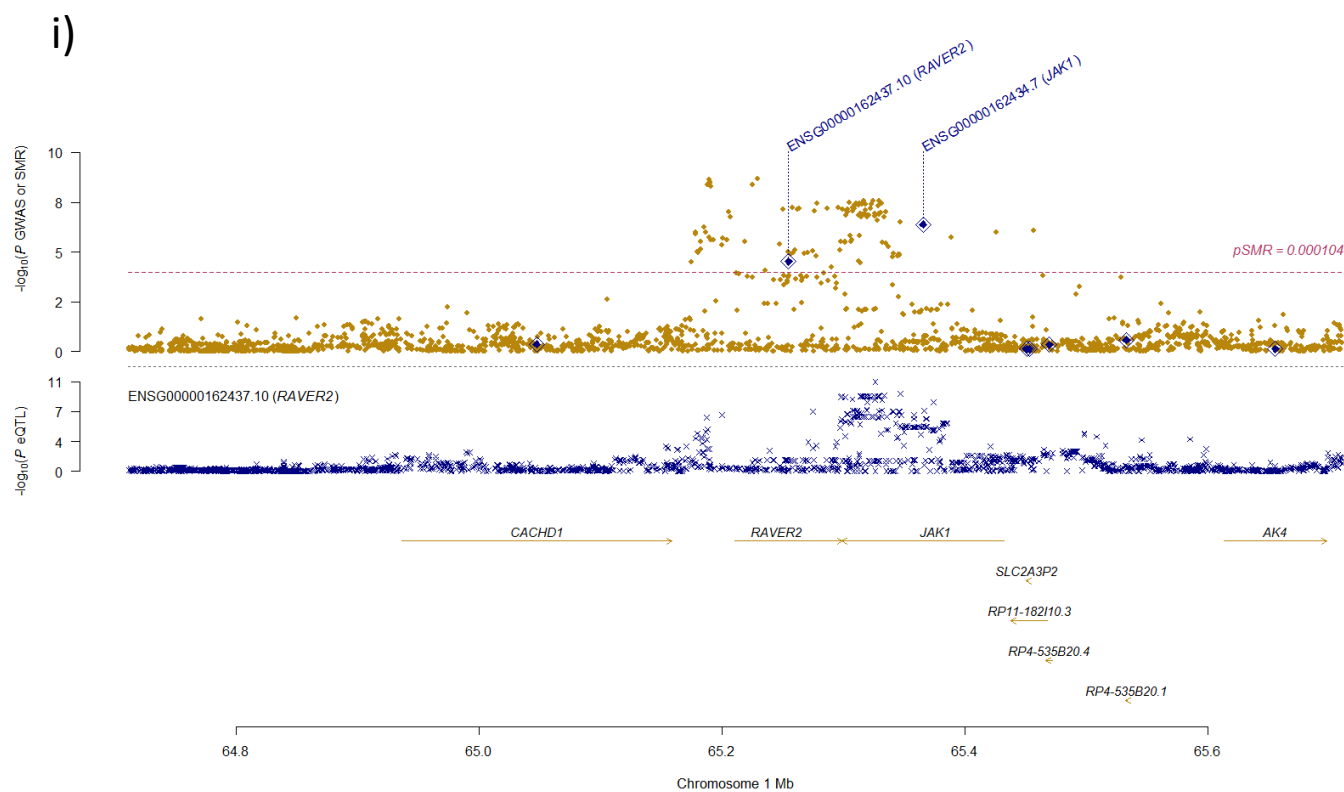
- (i) Upper panel - brown dots represent P -values for SNPs from the meta-analysis, diamonds represent P -values for probes from the SMR test, lower panel - crosses represent eQTL P -values of SNPs from respective tissue, genes passing the SMR (*i.e.* $P_{SMR} < 1.06 \times 10^{-4}$) and HEIDI (*i.e.* $P_{HEIDI} > 0.05$) tests are highlighted in red, the top and bottom plots include all SNPs mapping to the region in the GWAS and eQTL summary data, rather than only the SNPs common to both data sets
- (ii) Effect sizes of SNPs (used for the HEIDI test) from GWAS meta-analysis plotted against those for SNPs from the respective eQTL study. The orange dashed lines correspond to the estimate of b_{xy} at the top cis-eQTL. Error bars correspond to standard errors of SNP effects.

Note: the SMR method calculates eQTL P -values from beta and standard error values, therefore reported eQTL P -values may not coincide exactly with those reported by GTEx.

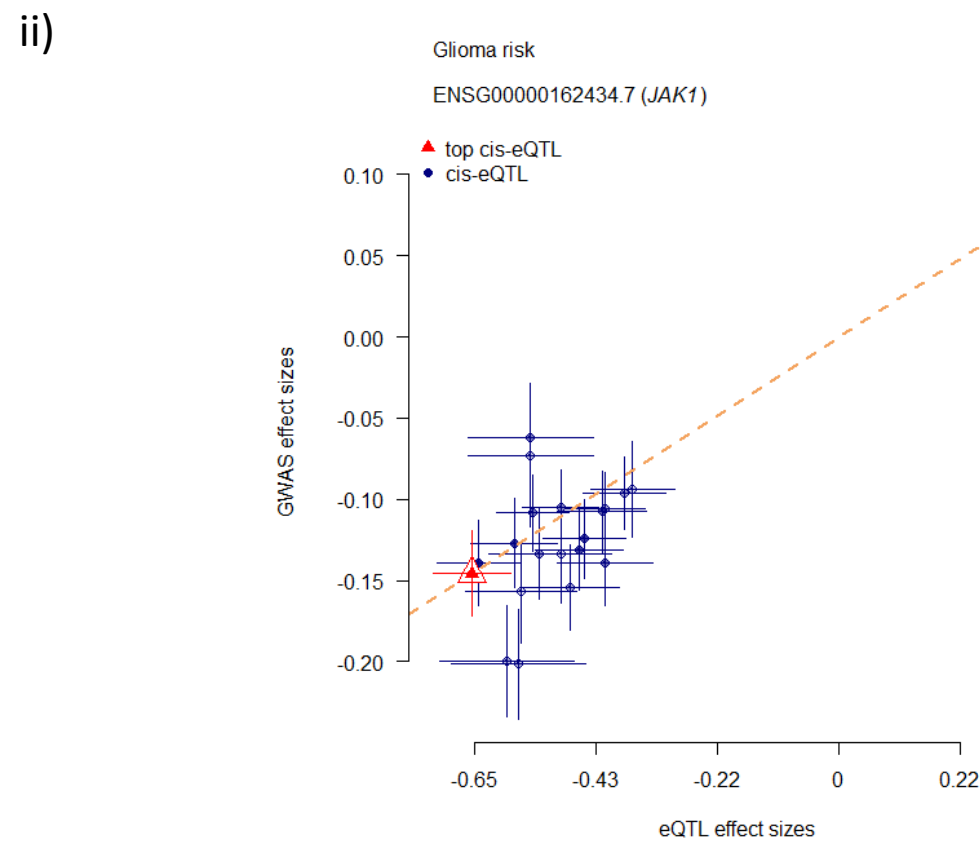
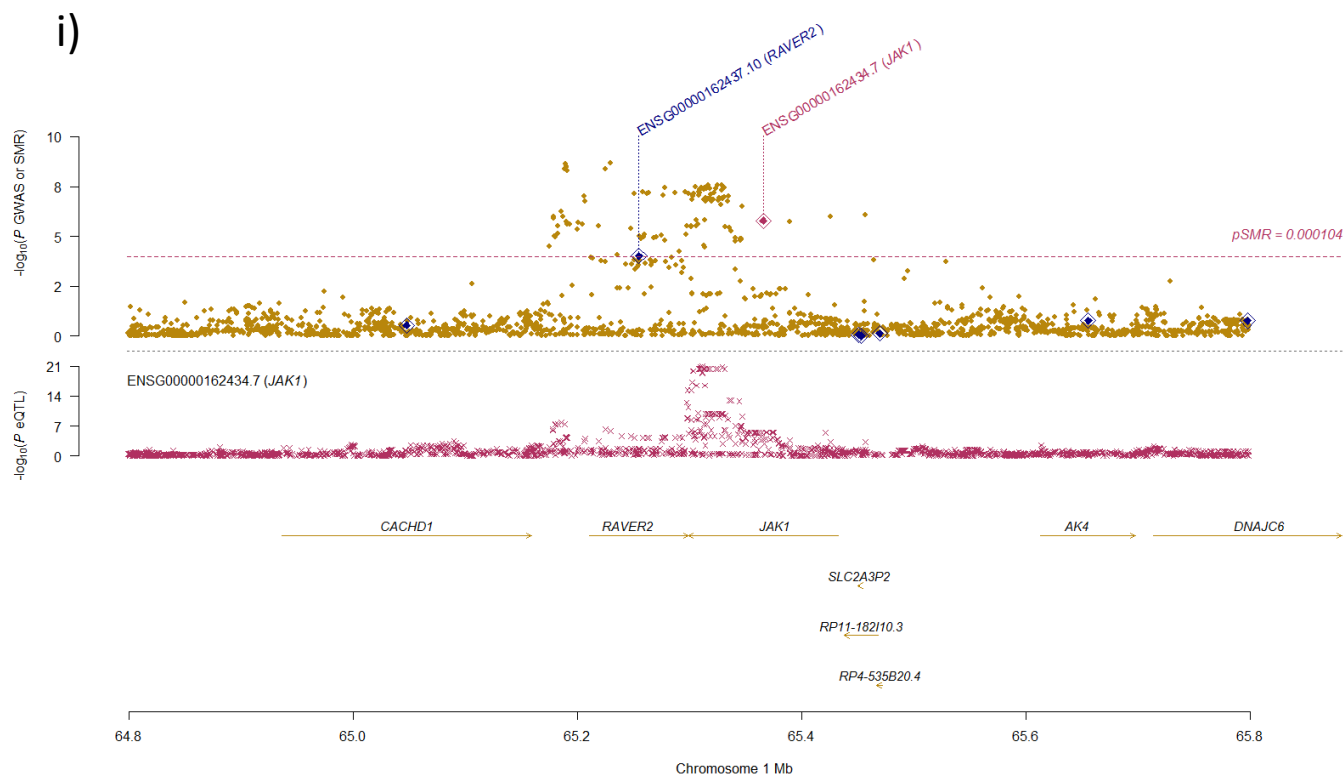
a) 1p31.3 (GBM) ENSG00000162434.7 (*JAK1*) Brain Cerebellum



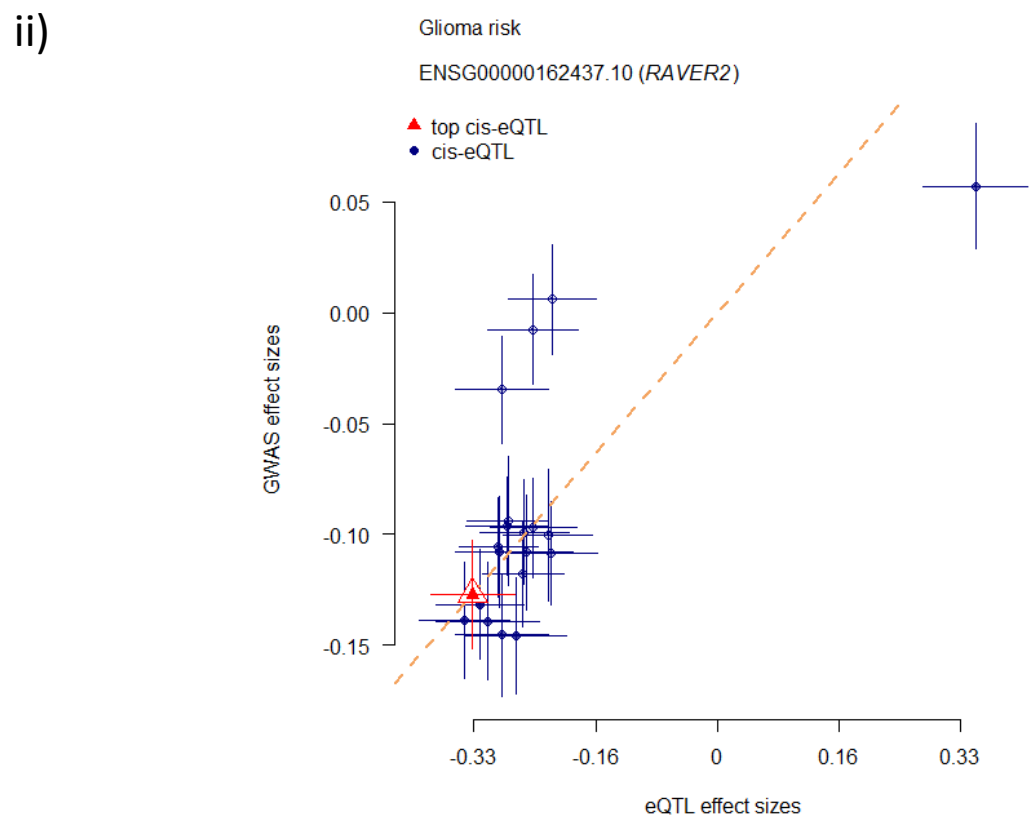
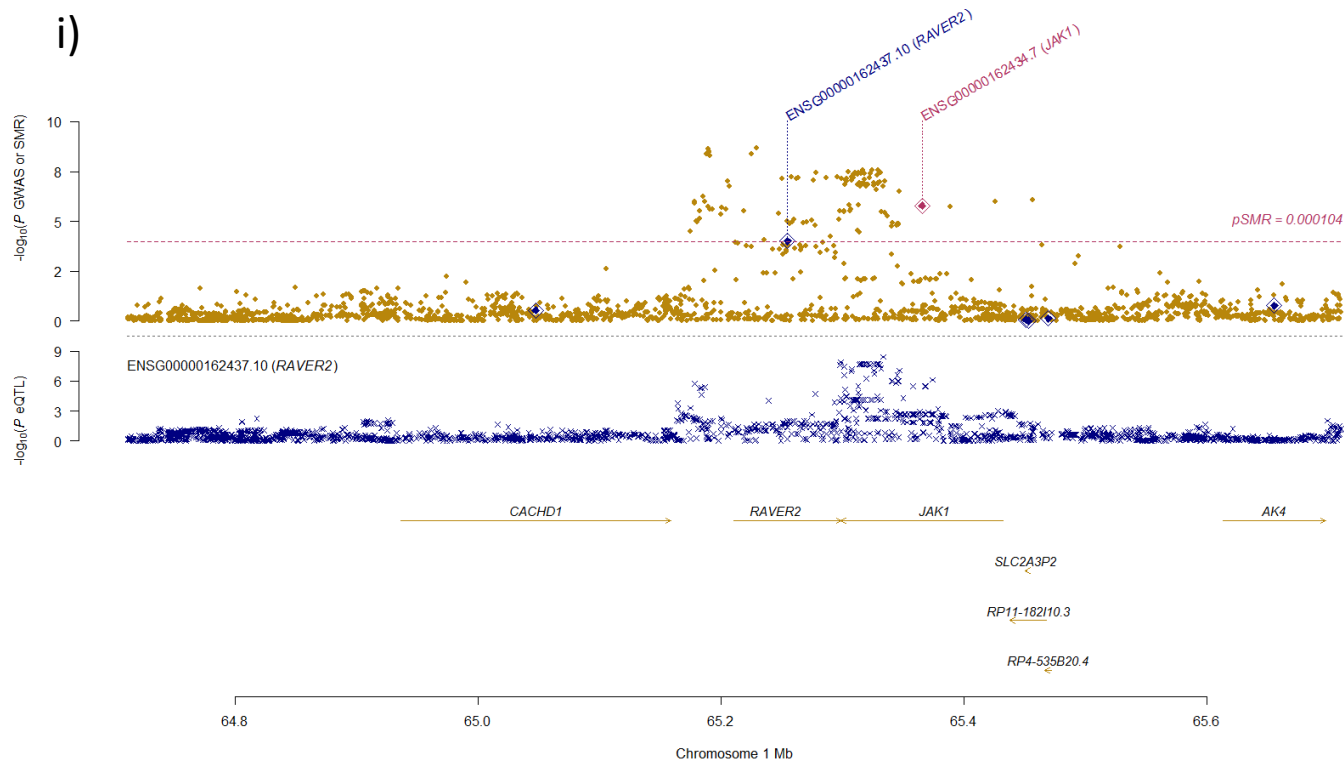
b) 1p31.3 (GBM) ENSG00000162437.10 (*RAVER2*) Brain Cerebellum



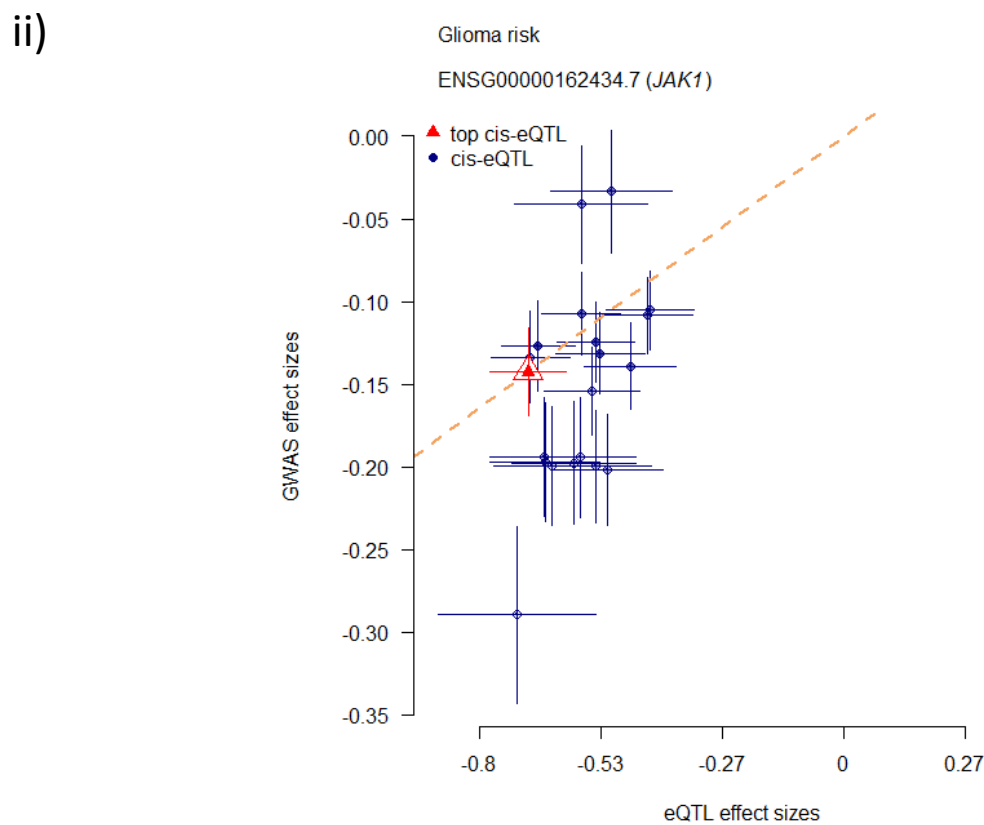
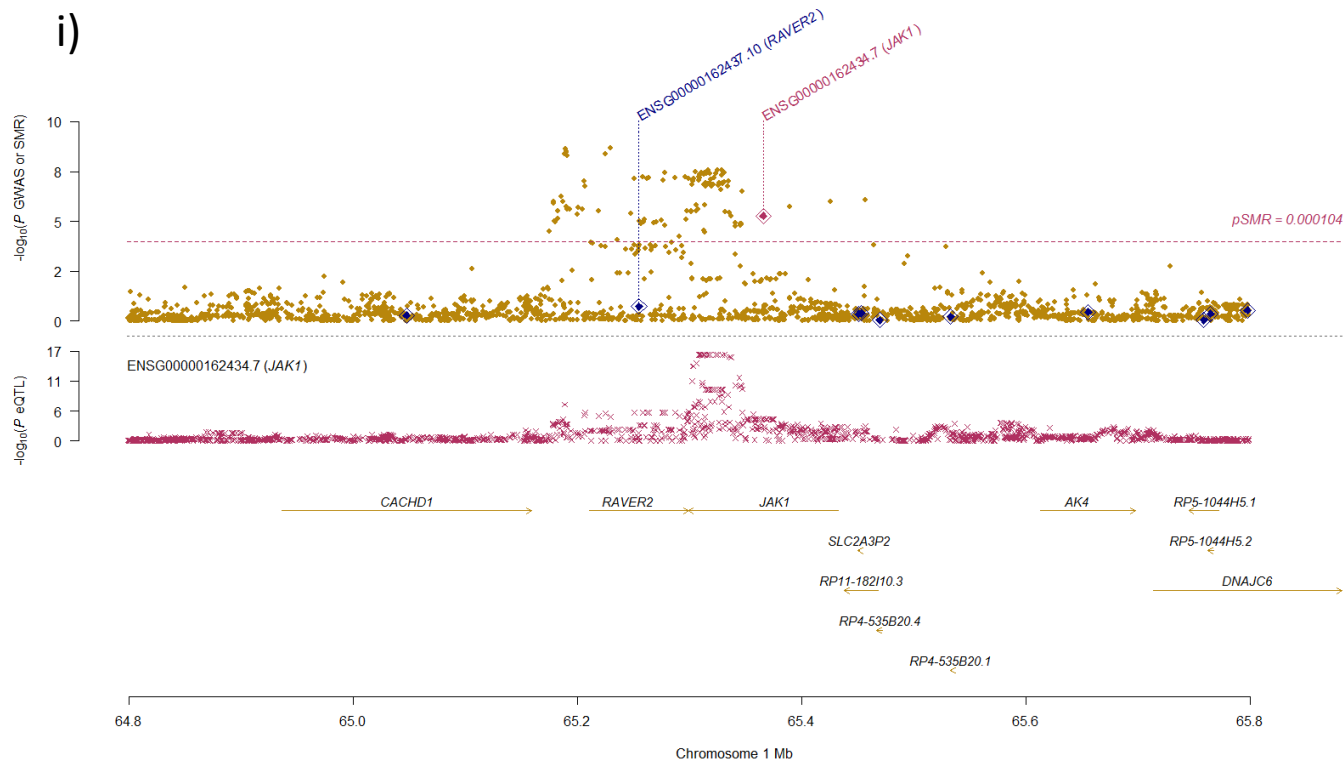
c) 1p31.3 (GBM) ENSG00000162434.7 (*JAK1*) Brain Cortex



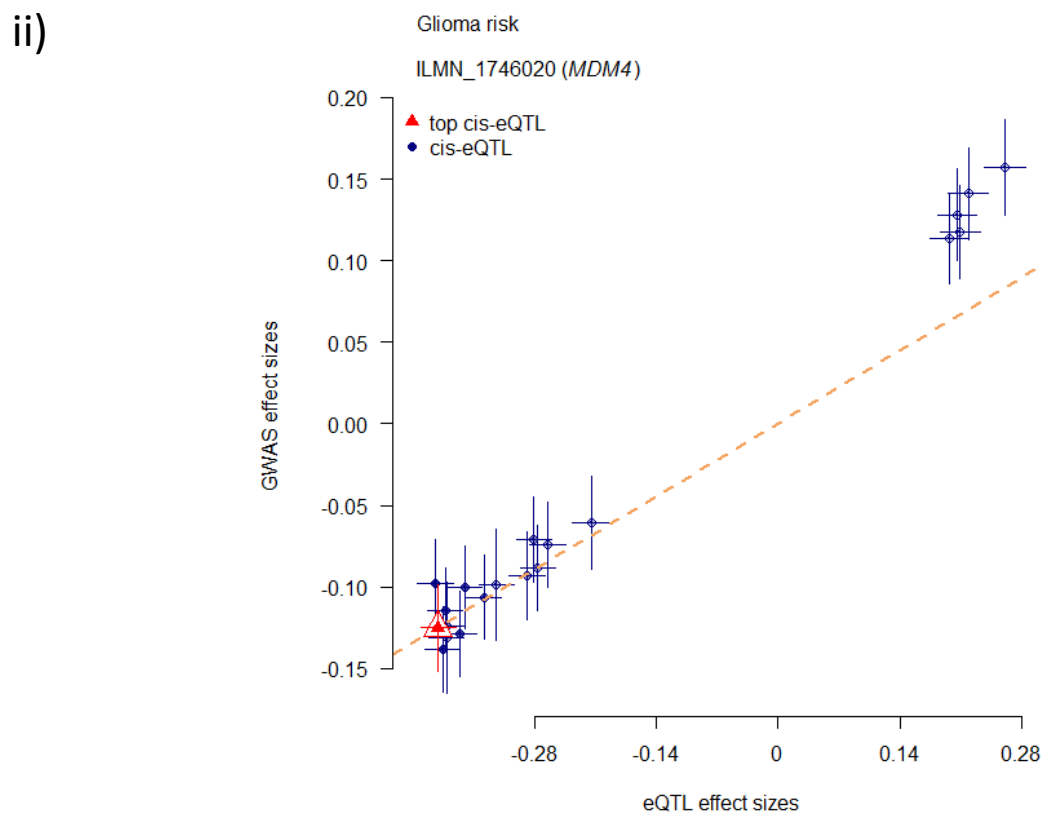
d) 1p31.3 (GBM) ENSG00000162437.10 (*RAVER2*) Brain Cortex



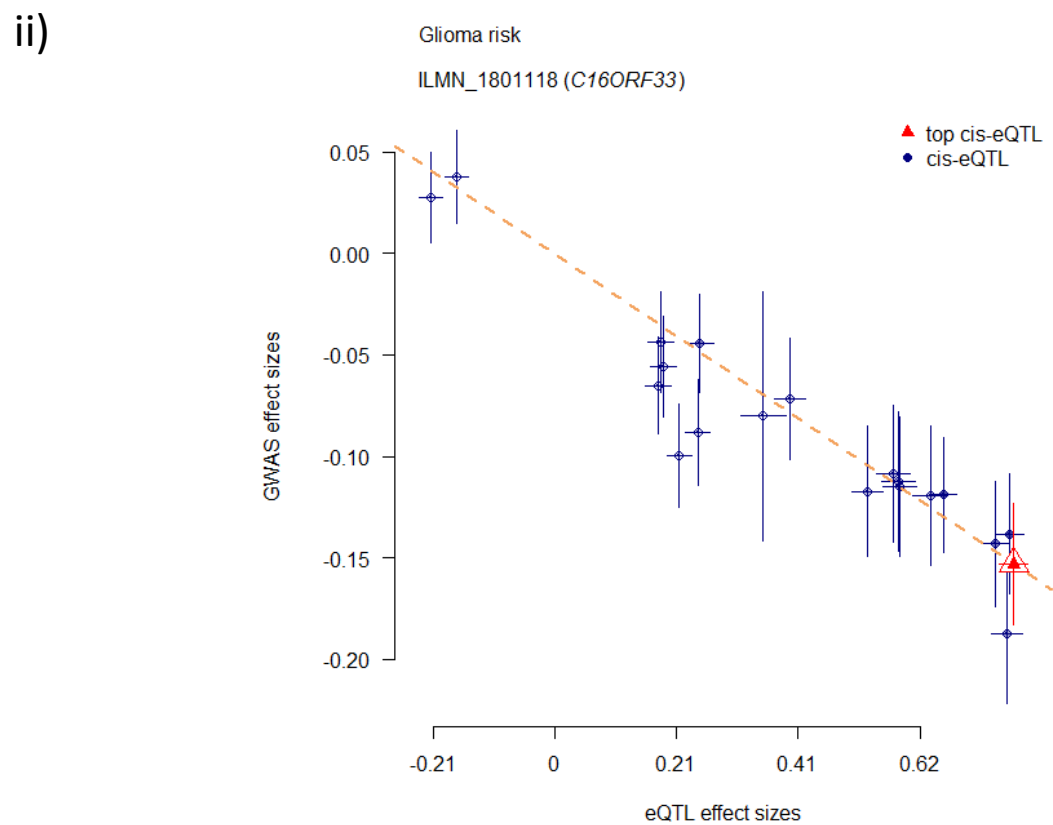
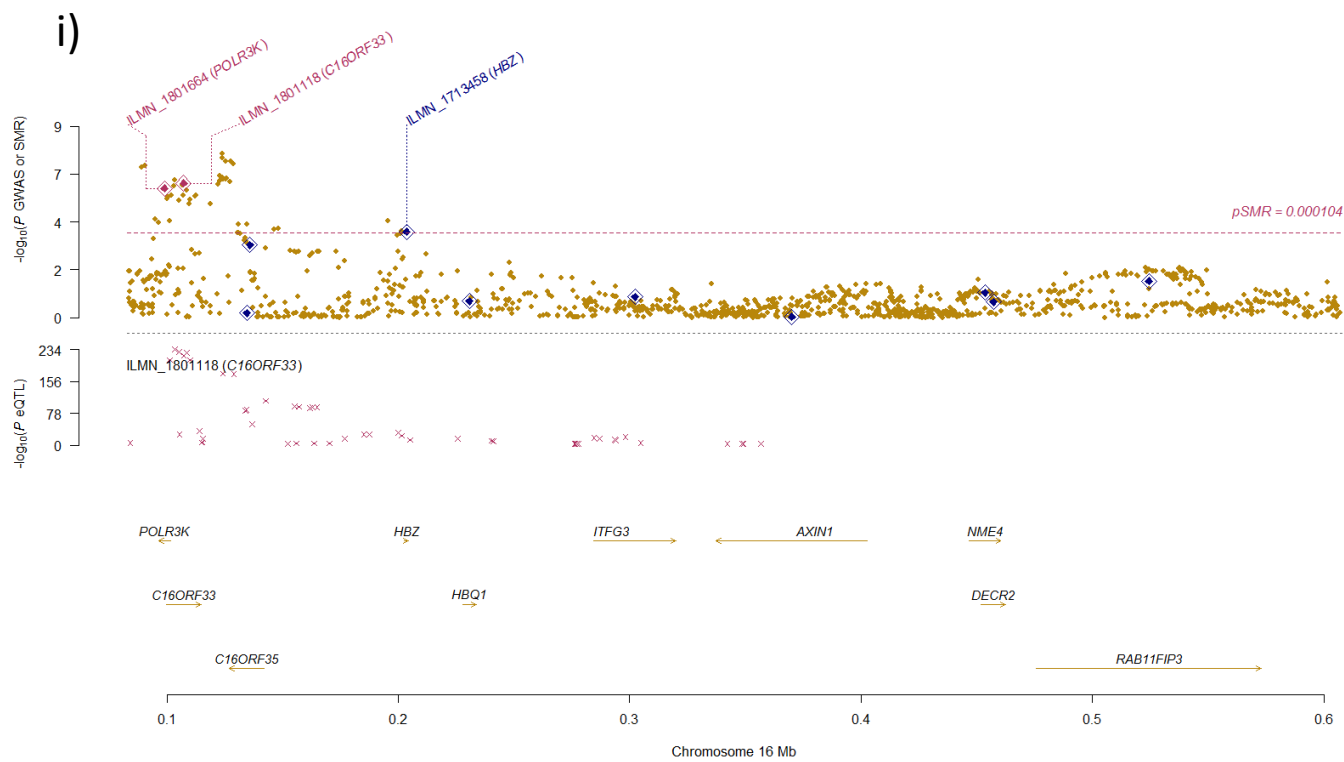
e) 1p31.3 (GBM) ENSG00000162434.7 (*JAK1*)
Brain Cerebellar Hemisphere



f) 1q32.1 (non-GBM) ILMN_1746020 (*MDM4*) Whole Blood

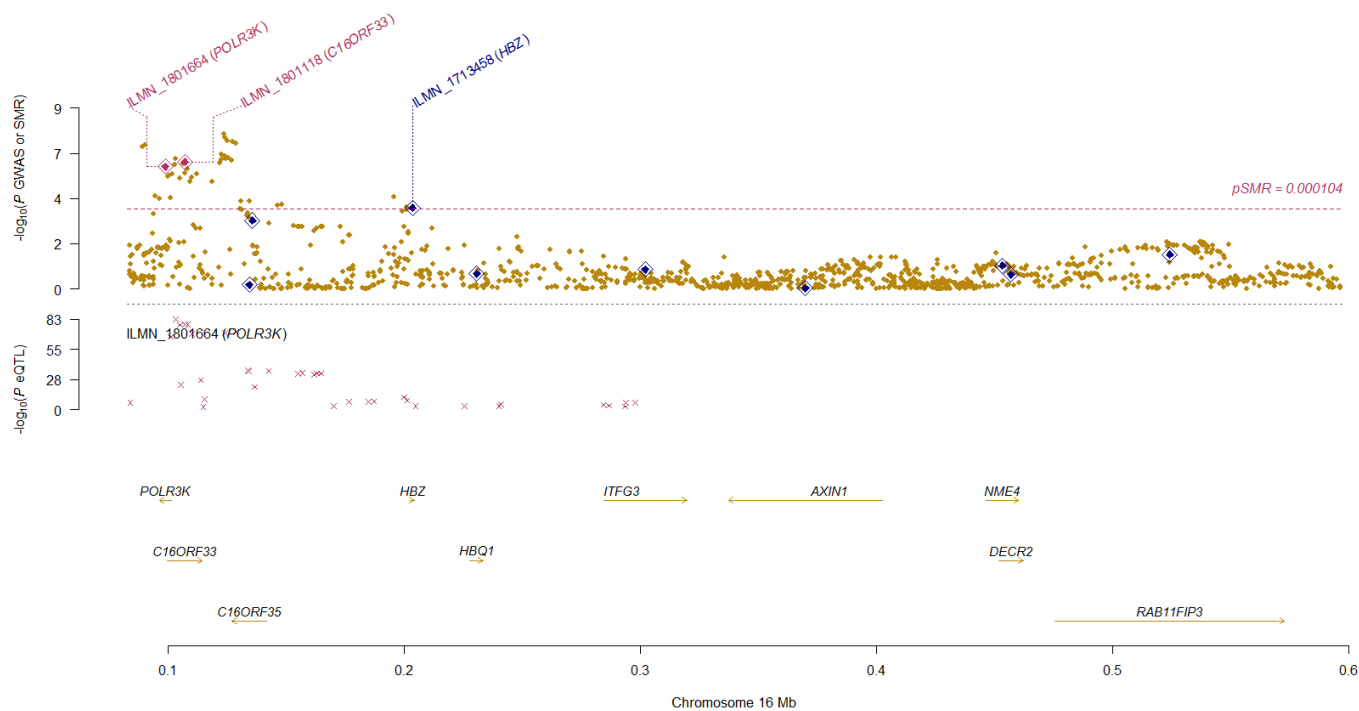


g) 16p13.3 (GBM) ILMN_1801118 (*C16ORF33*) Whole Blood

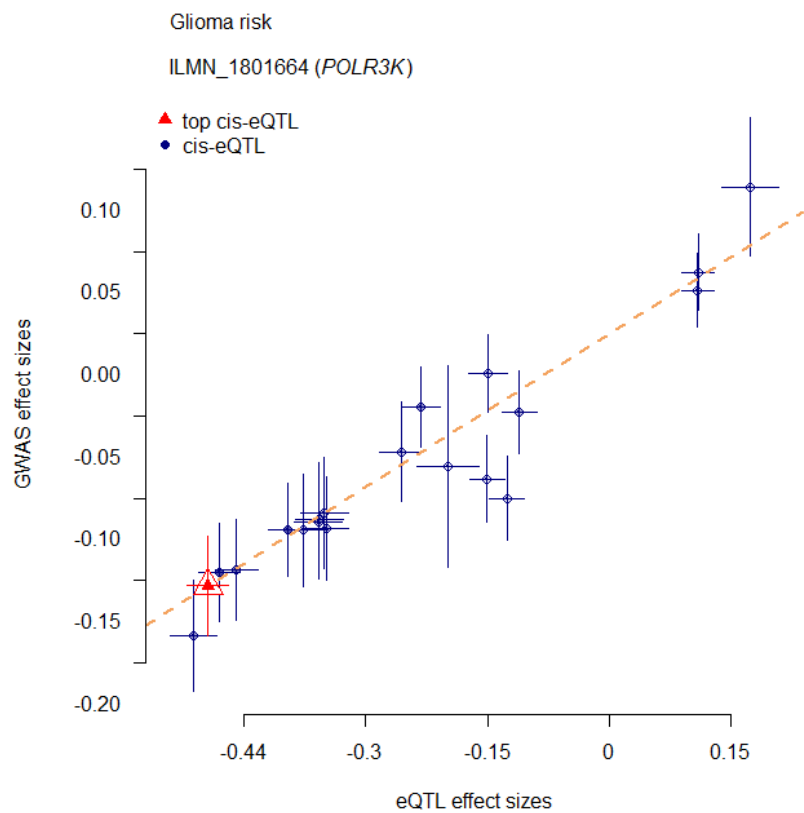


h) 16p13.3 (GBM) ILMN_1801664 (*POLR3K*) Whole Blood

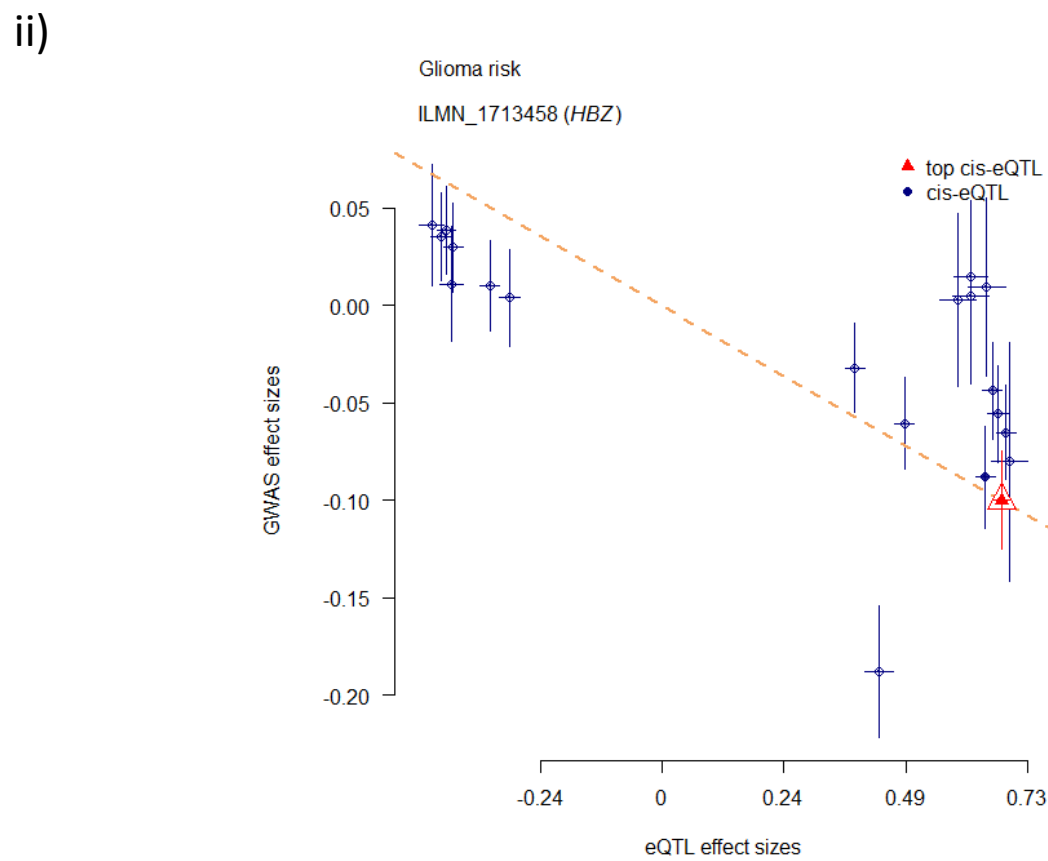
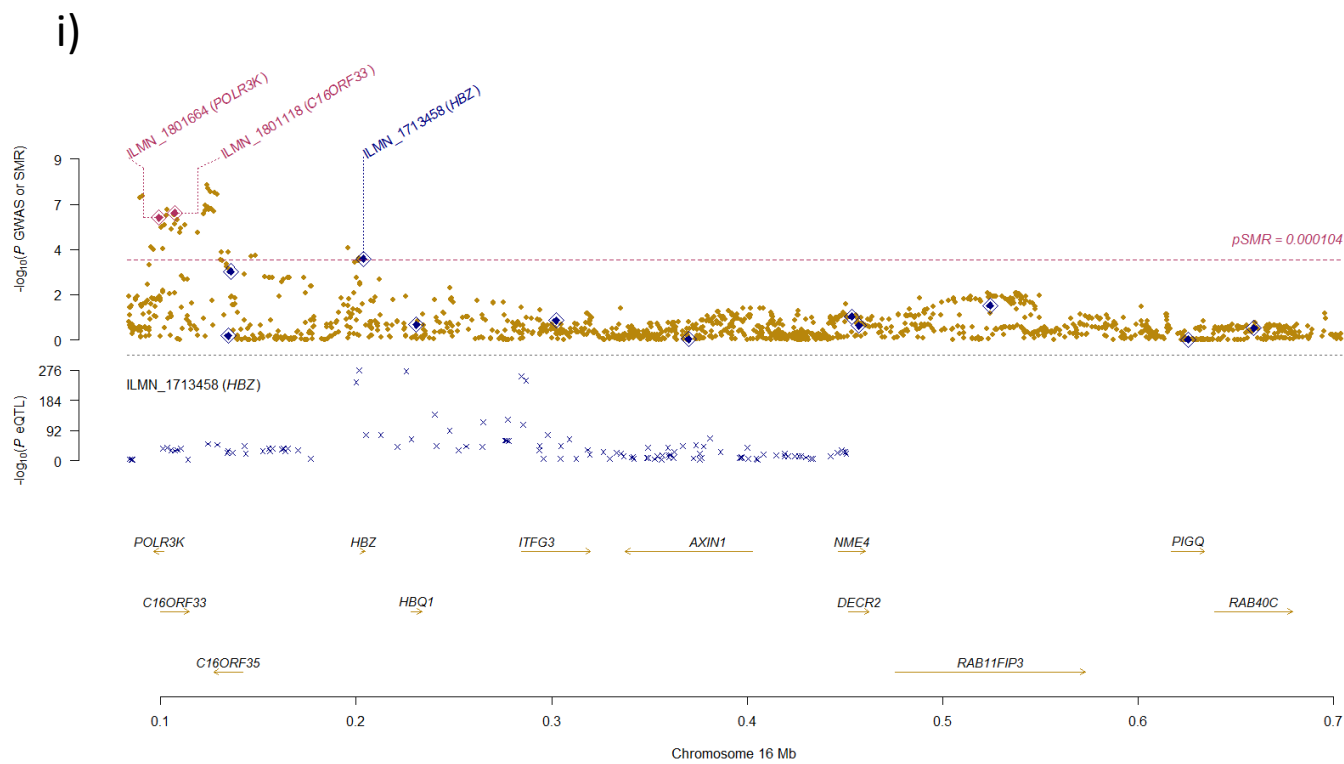
i)



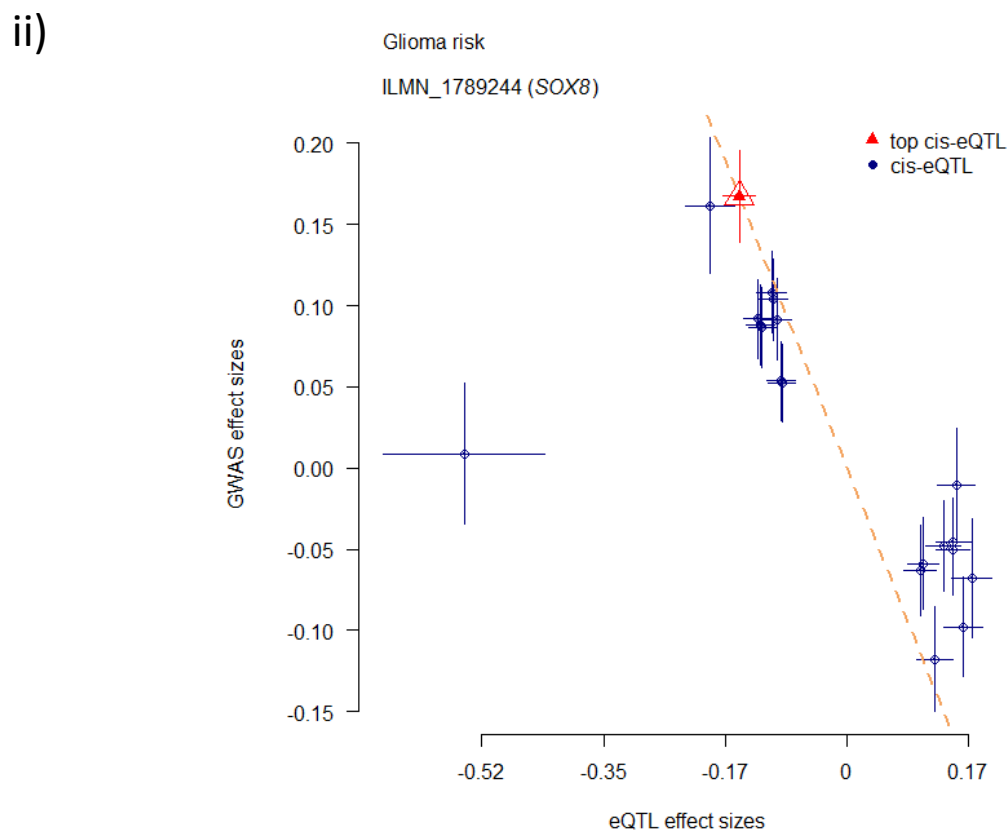
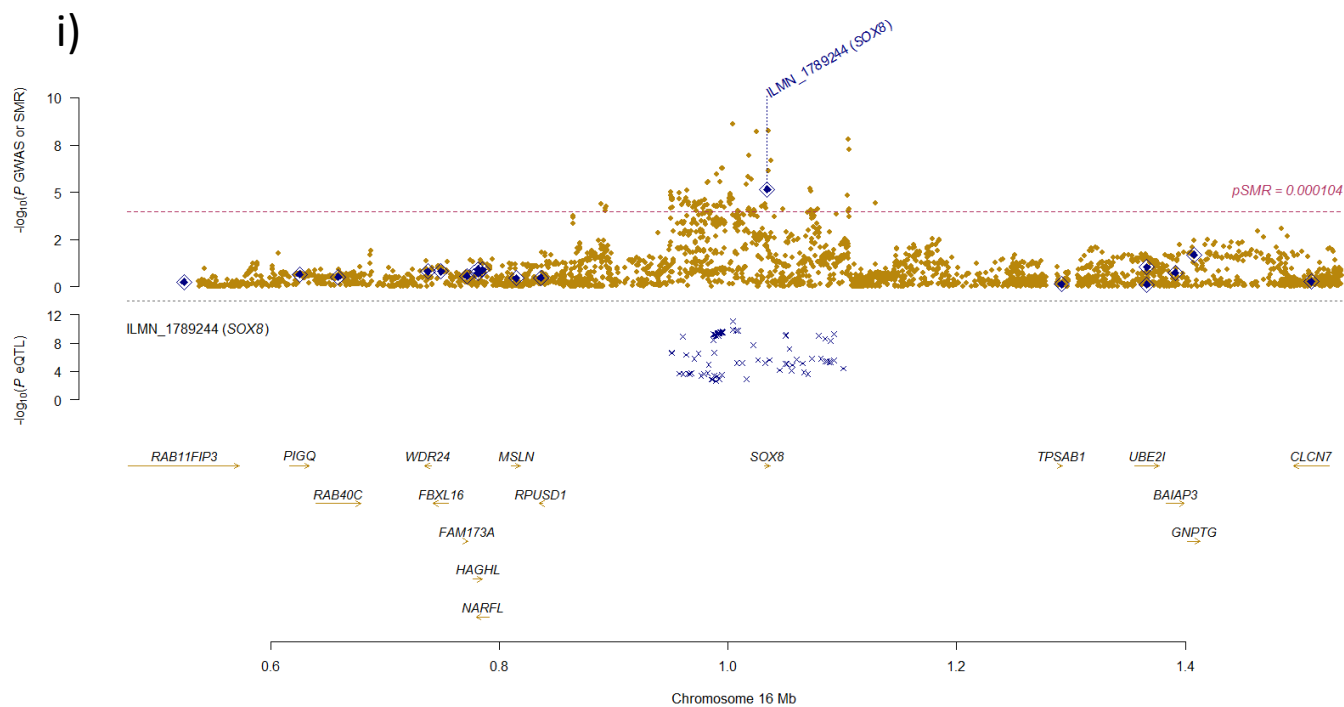
ii)



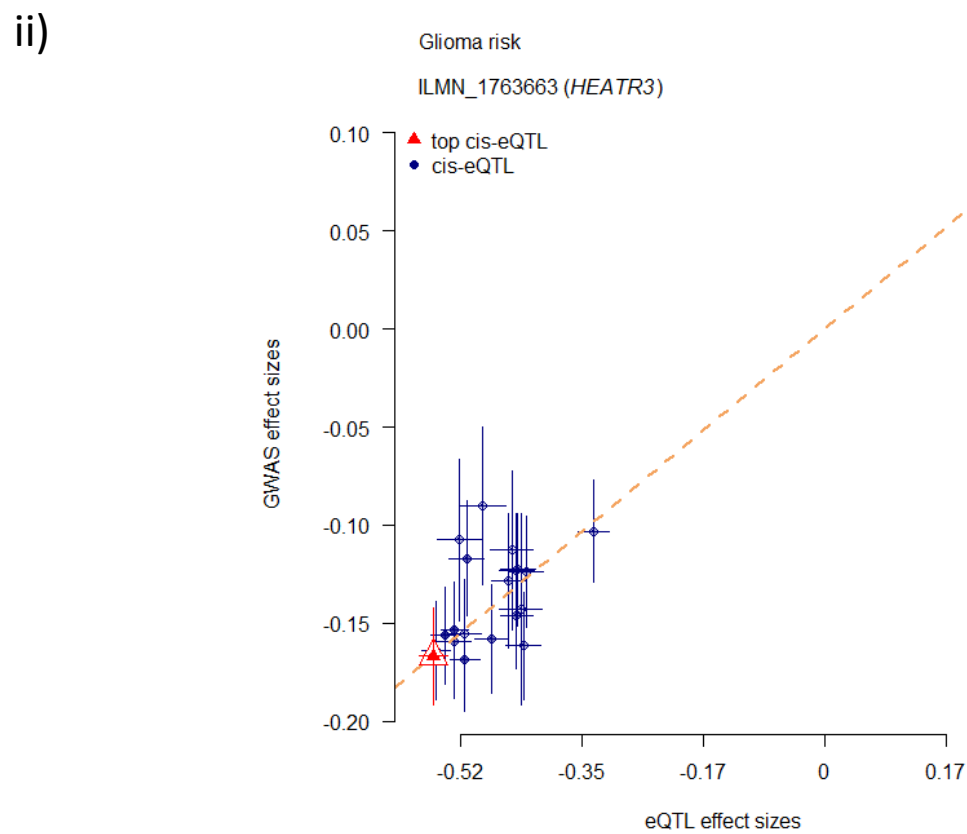
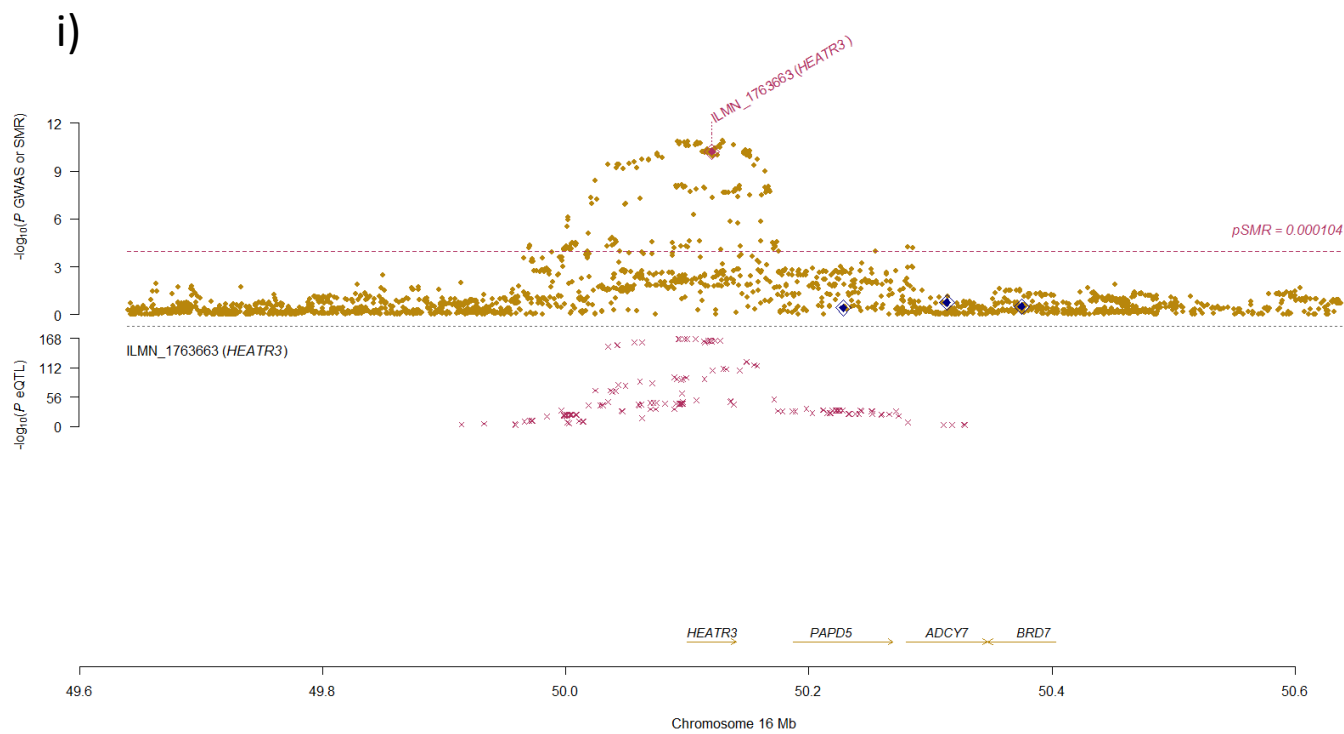
i) 16p13.3 (GBM) ILMN_1713458 (HBZ) Westra Whole Blood



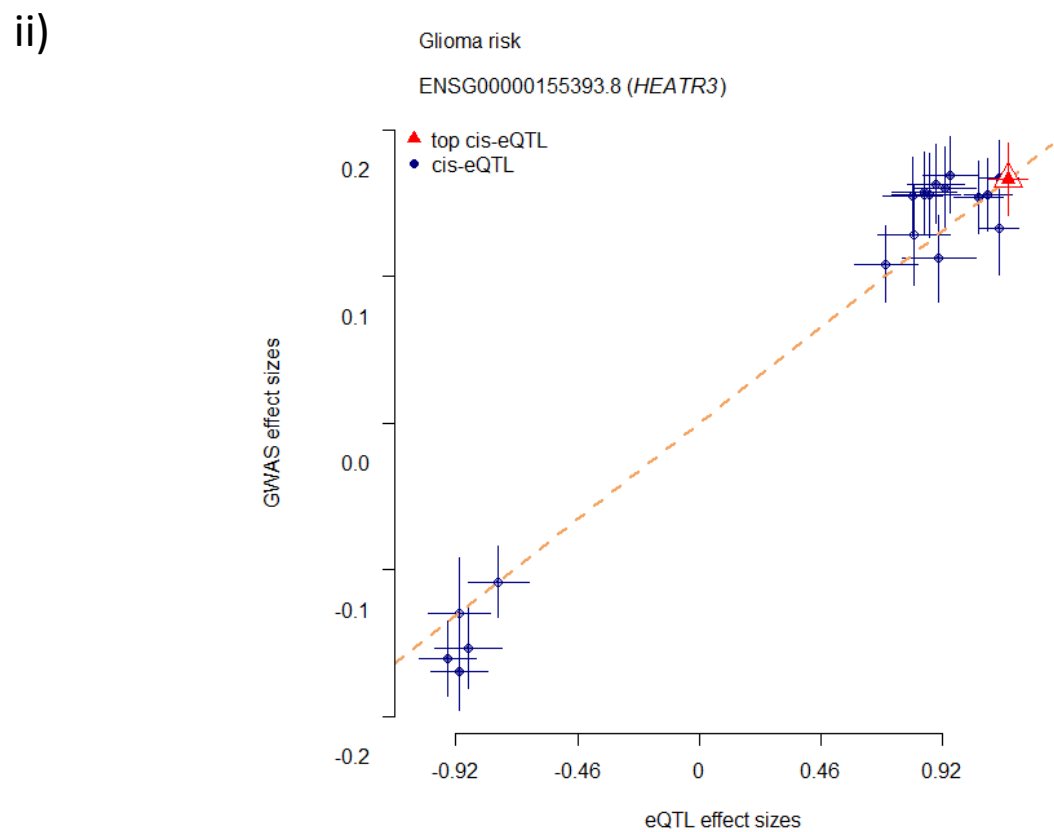
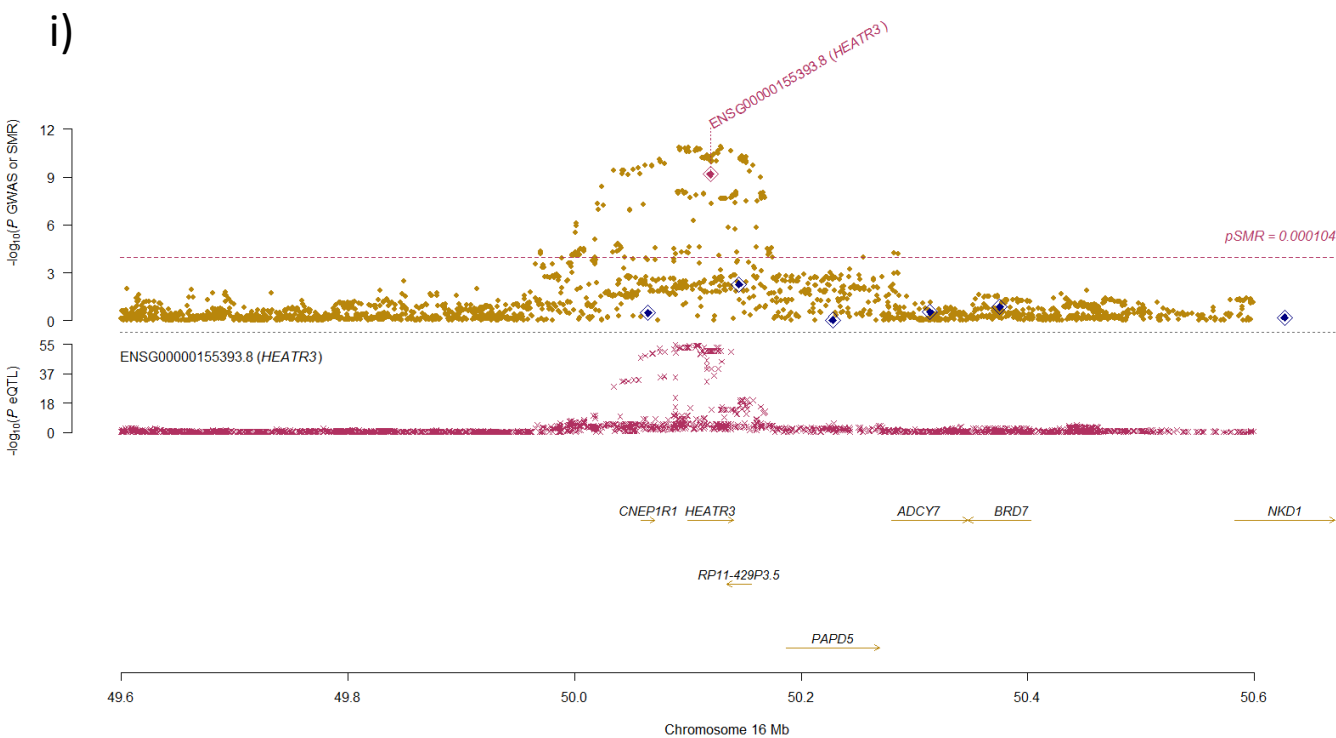
j) 16p13.3 (non-GBM) ILMN_1789244 (SOX8) Whole Blood



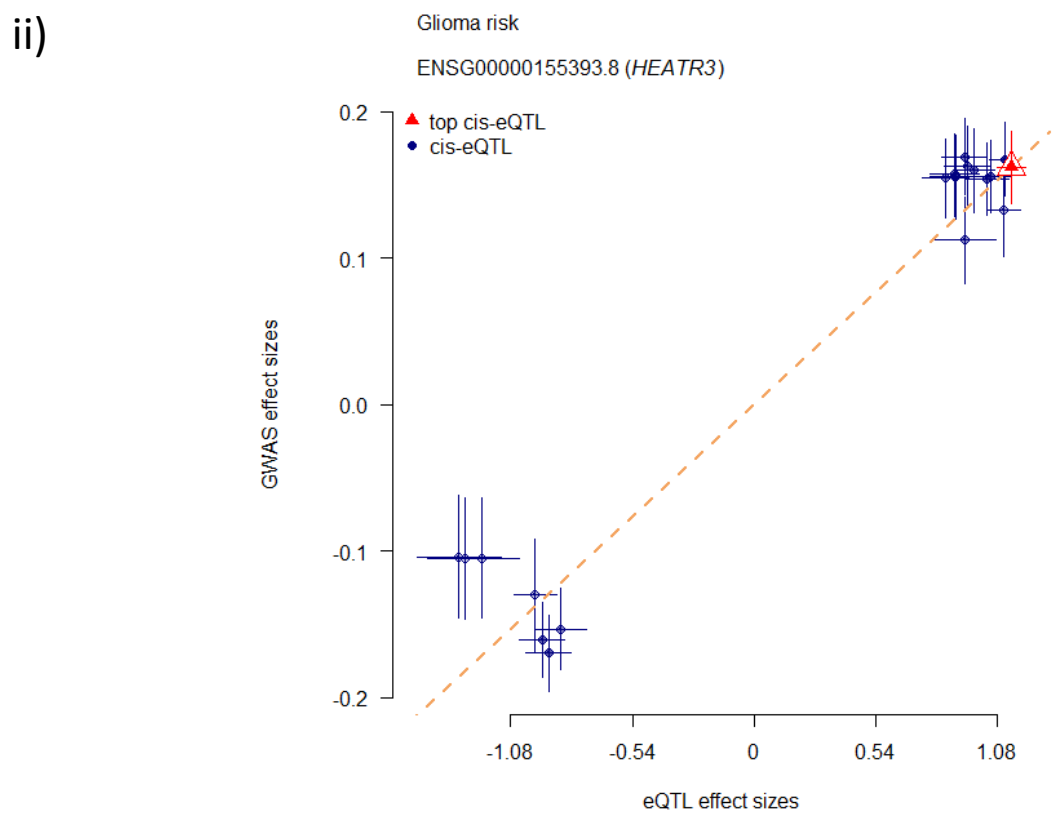
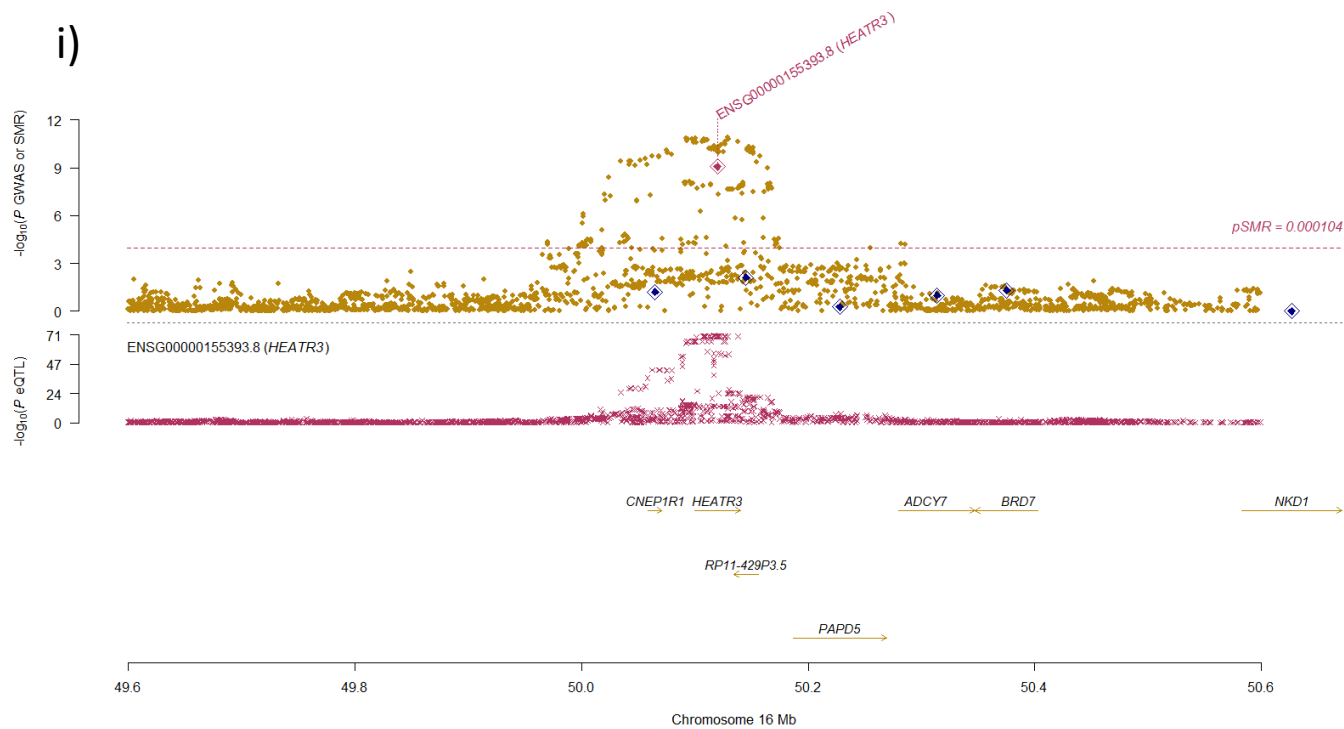
k) 16q12.1 (GBM) ILMN_1763663 (*HEATR3*) Whole Blood



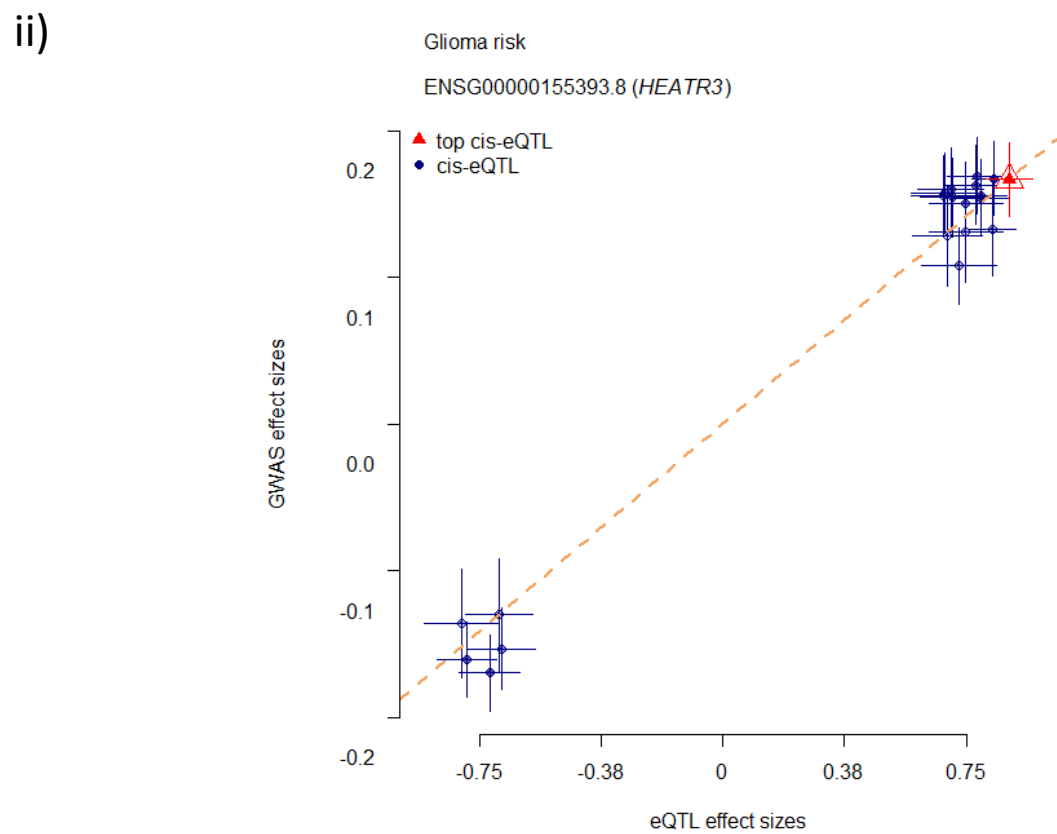
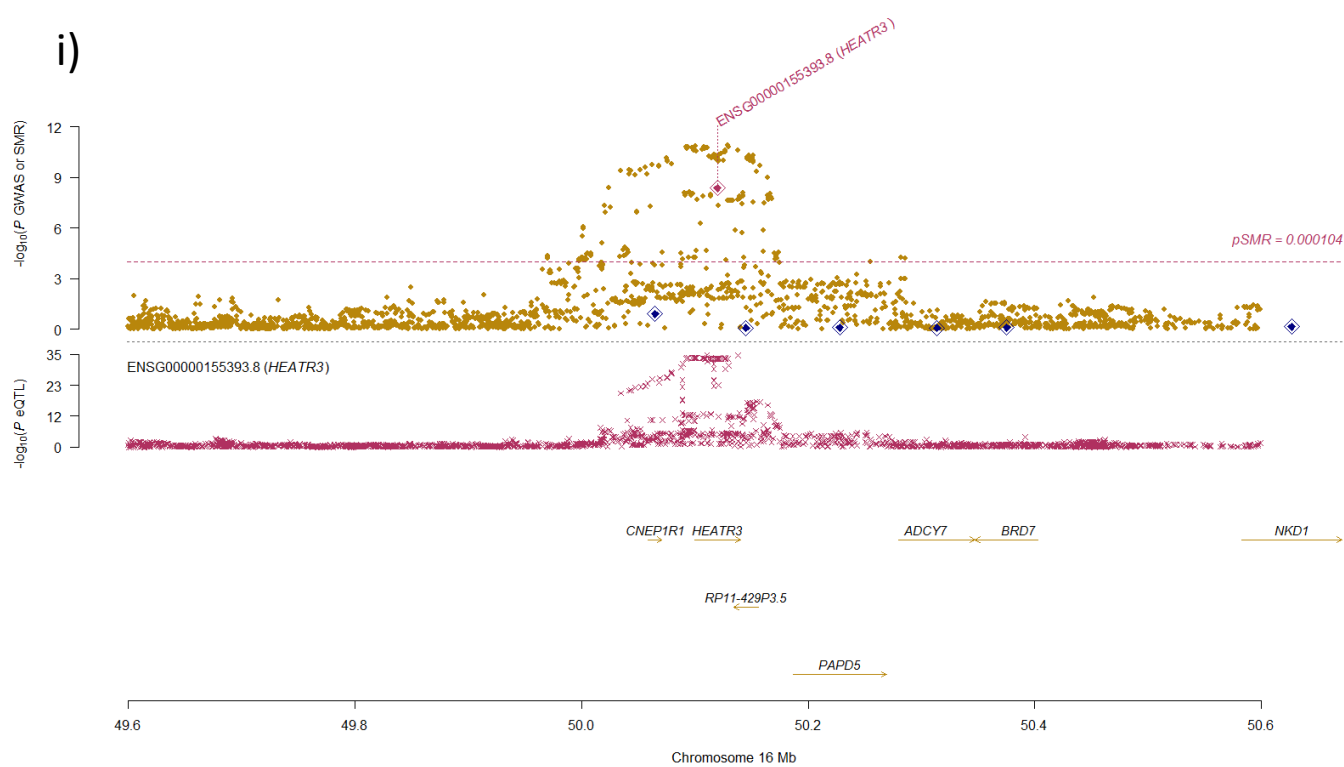
I) 16q12.1 (GBM) ENSG00000155393.8 (*HEATR3*)
Brain Cerebellar Hemisphere



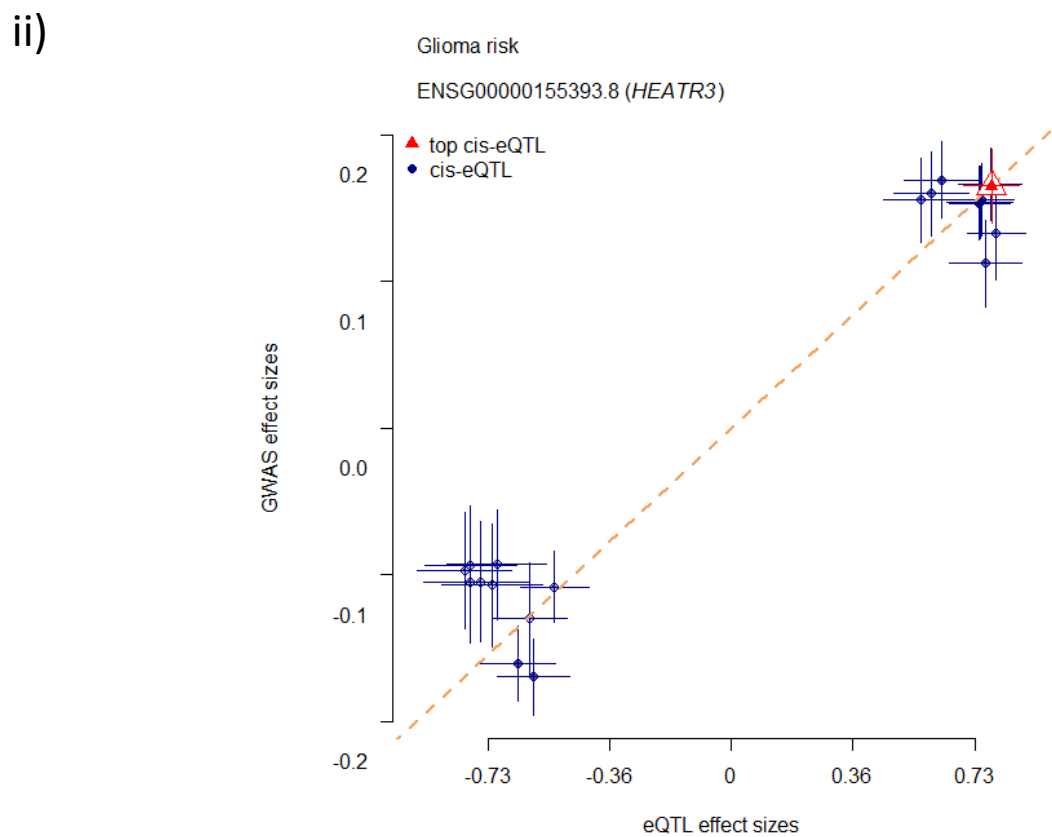
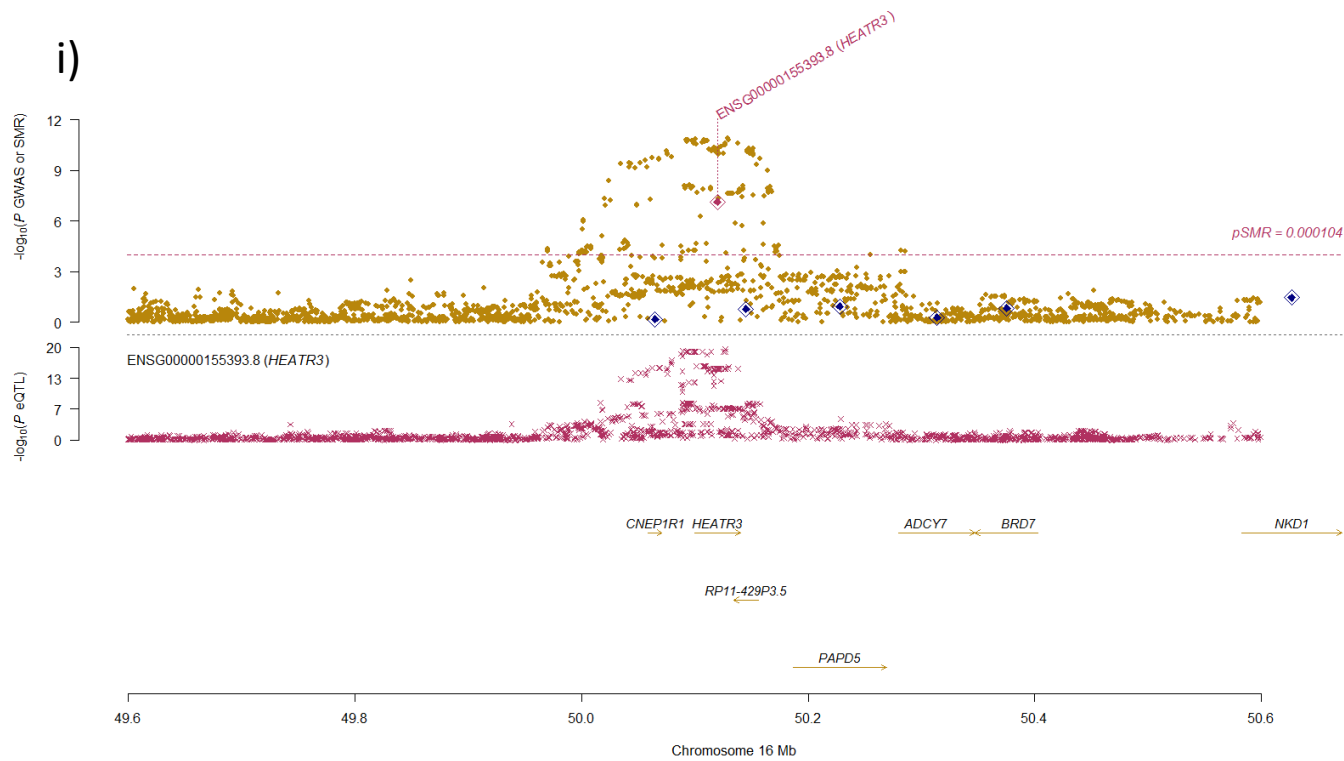
m) 16q12.1 (GBM) ENSG00000155393.8 (*HEATR3*)
Brain Cerebellum



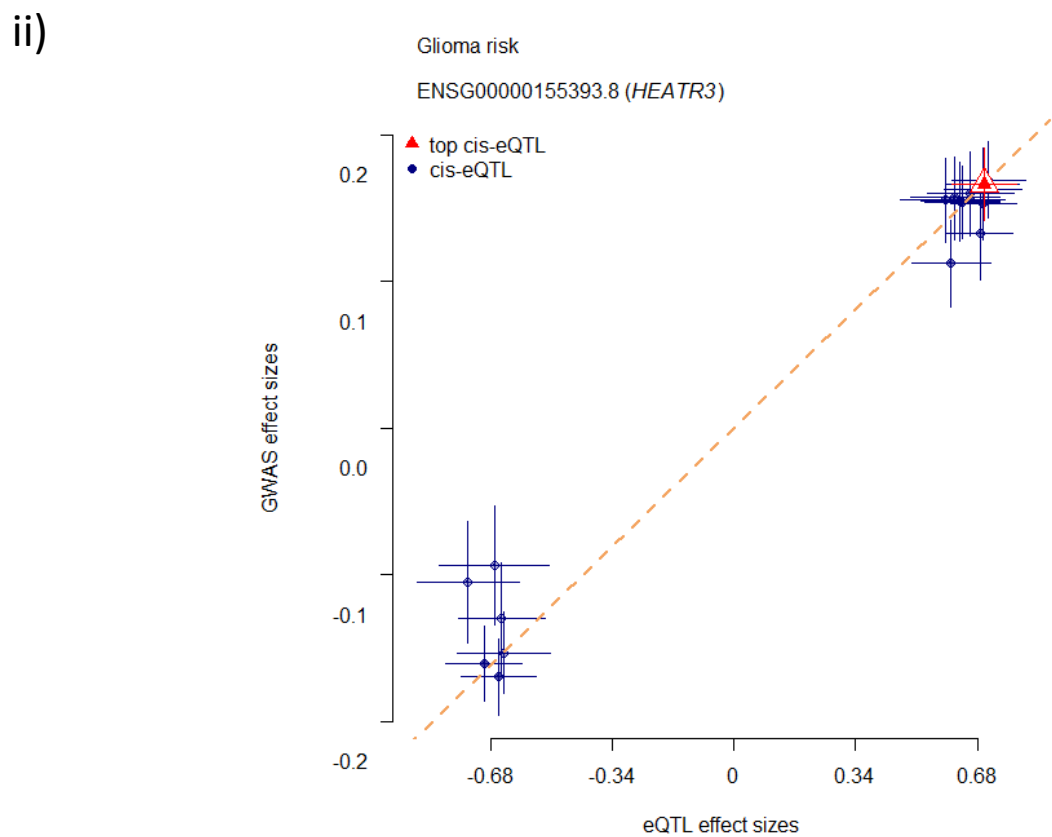
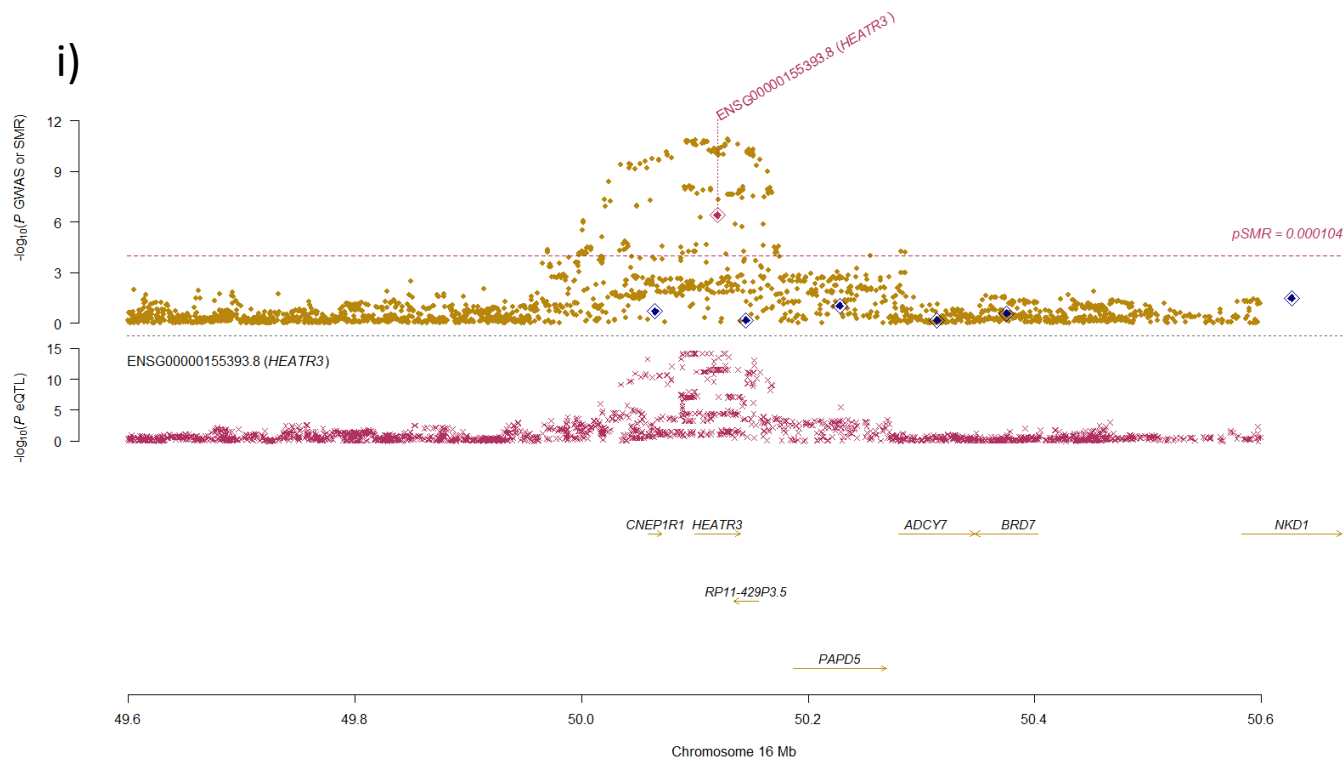
n) 16q12.1 (GBM) ENSG00000155393.8 (*HEATR3*) Brain Cortex



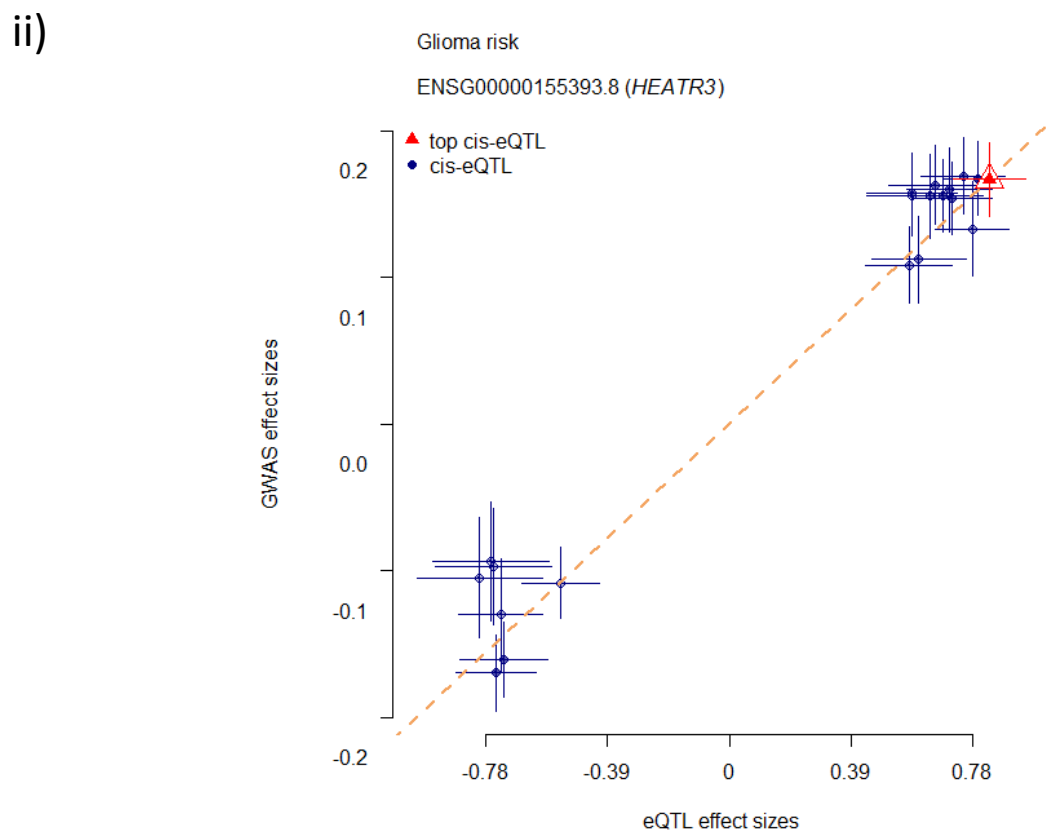
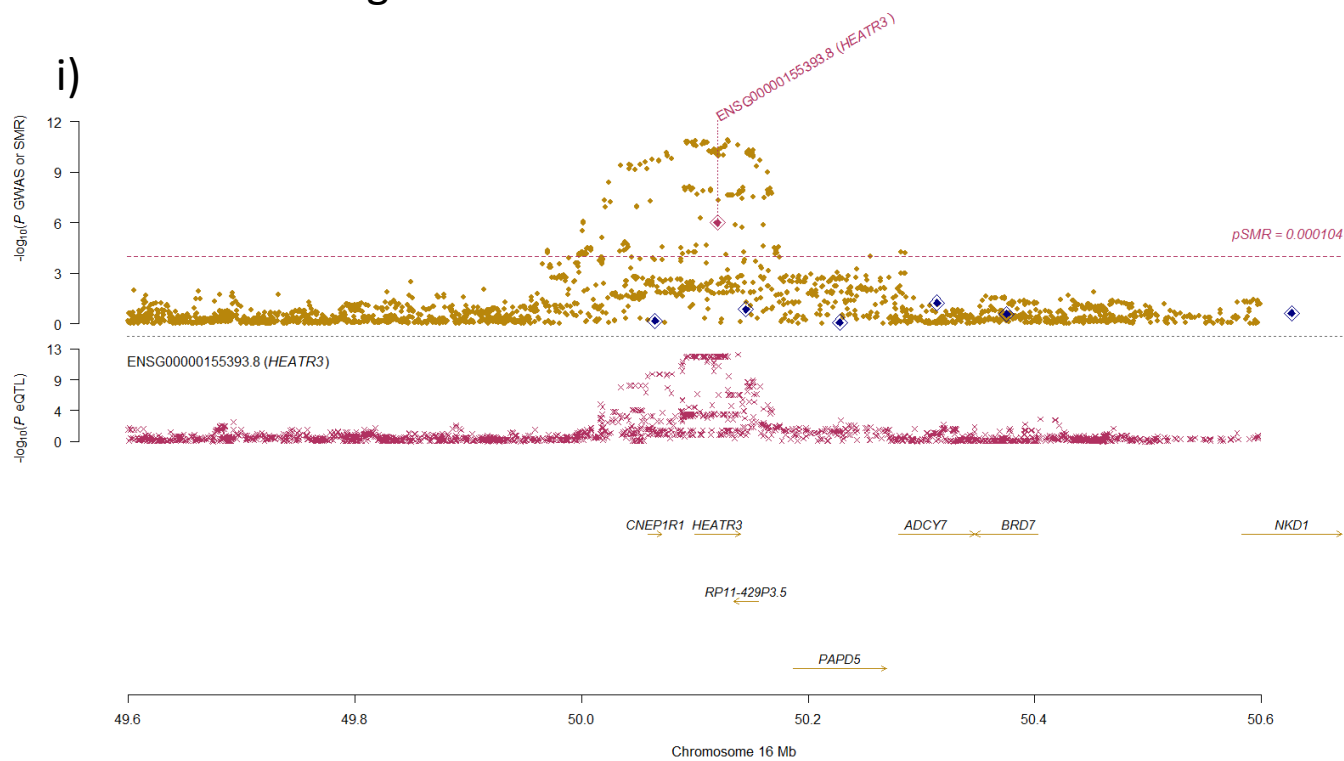
o) 16q12.1 (GBM) ENSG00000155393.8 (*HEATR3*)
Brain Nucleus accumbens basal ganglia



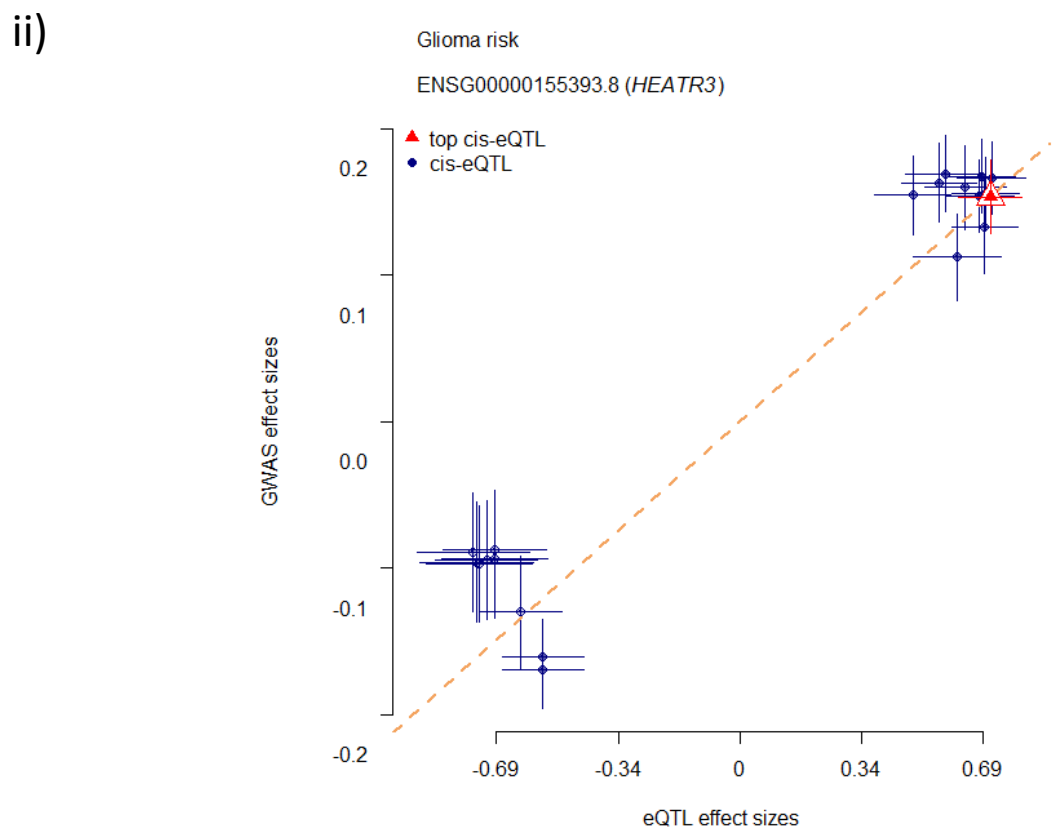
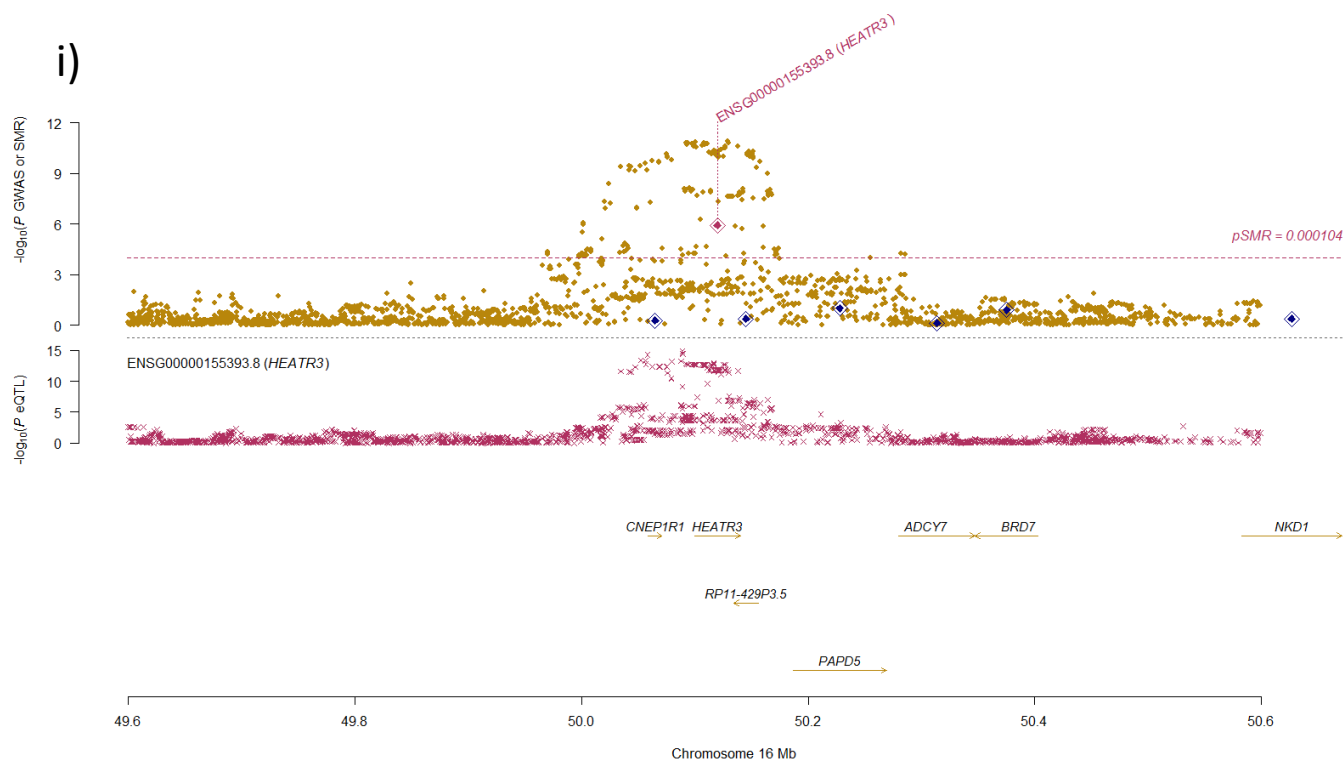
p) 16q12.1 (GBM) ENSG00000155393.8 (*HEATR3*)
Brain Frontal Cortex BA9



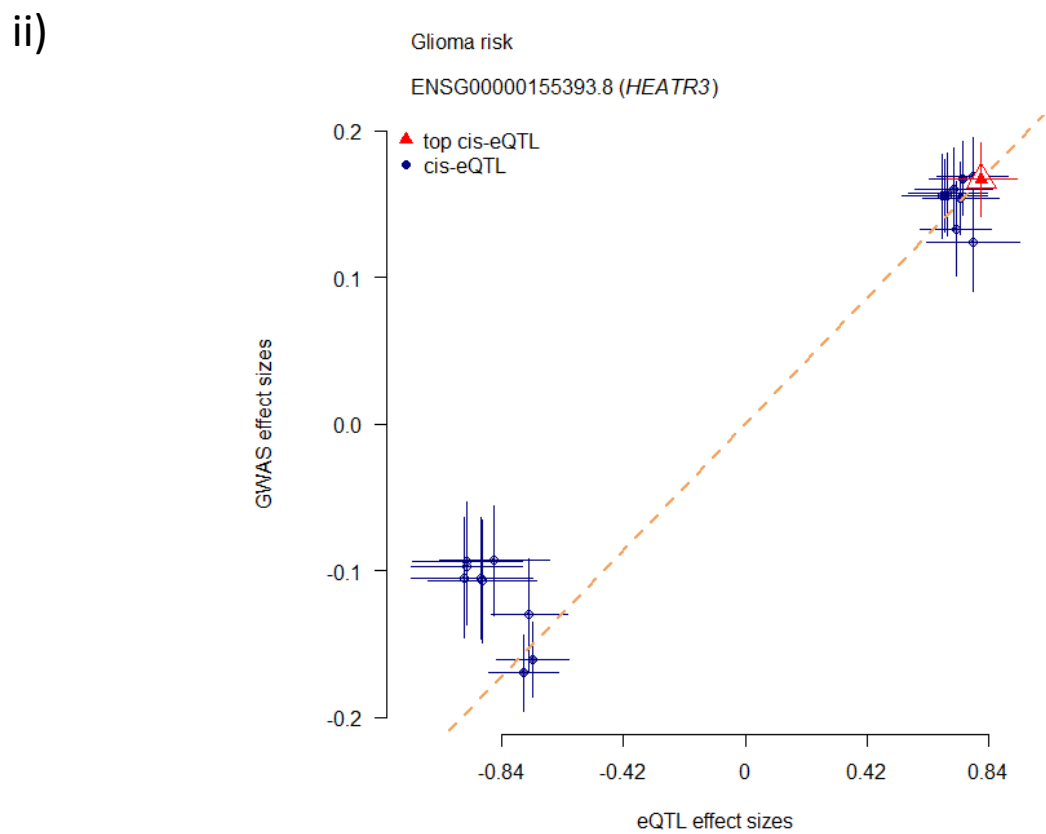
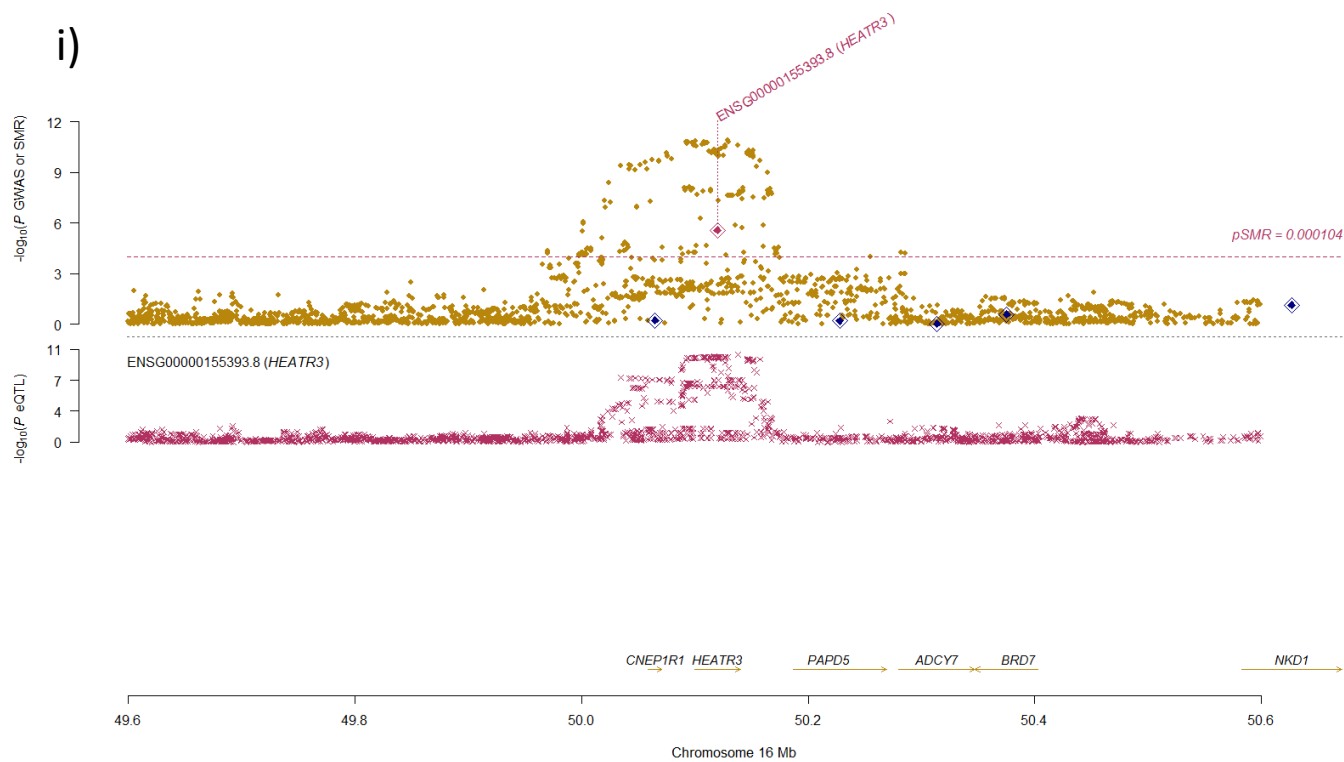
q) 16q12.1 (GBM) ENSG00000155393.8 (*HEATR3*)
Brain Anterior cingulate cortex BA24



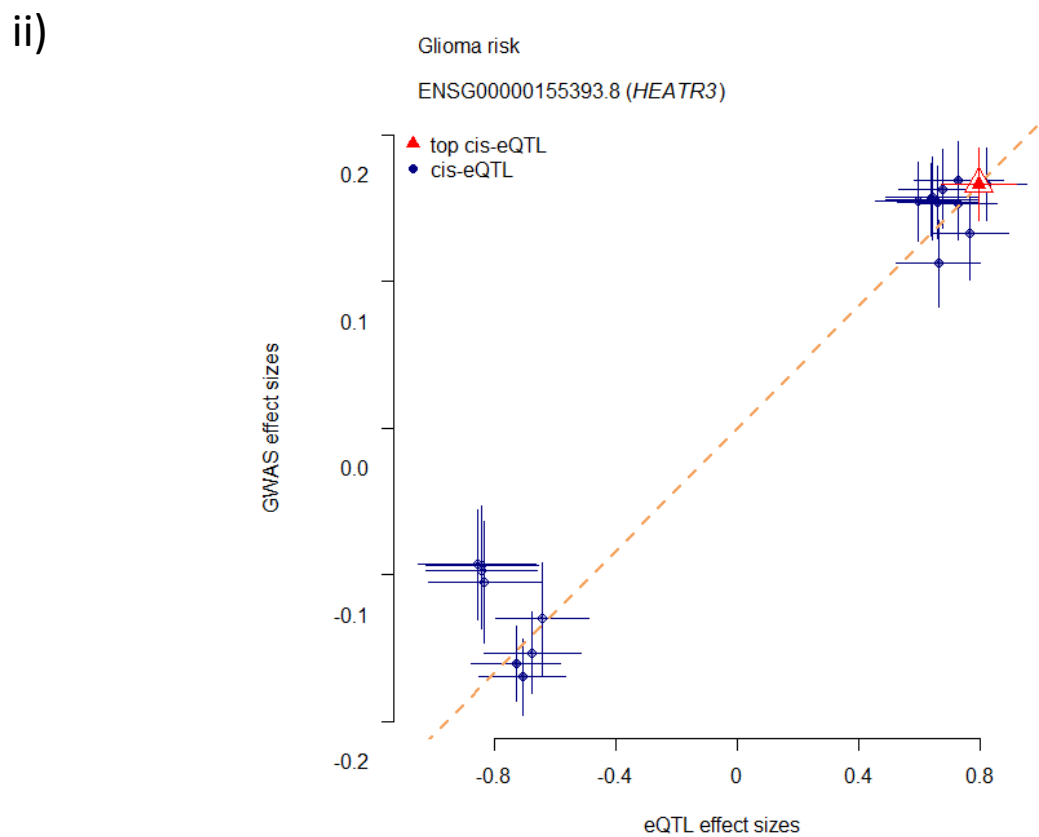
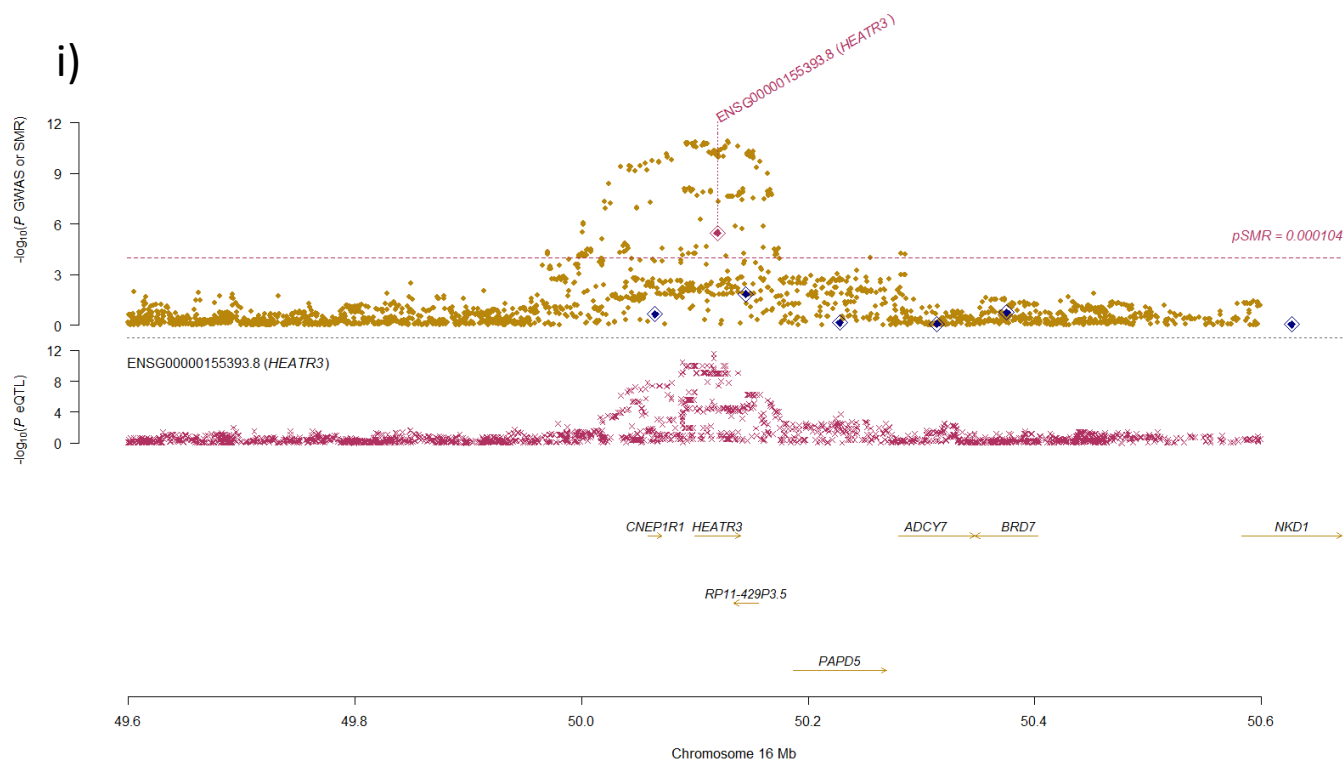
r) 16q12.1 (GBM) ENSG00000155393.8 (*HEATR3*)
Brain Putamen basal ganglia



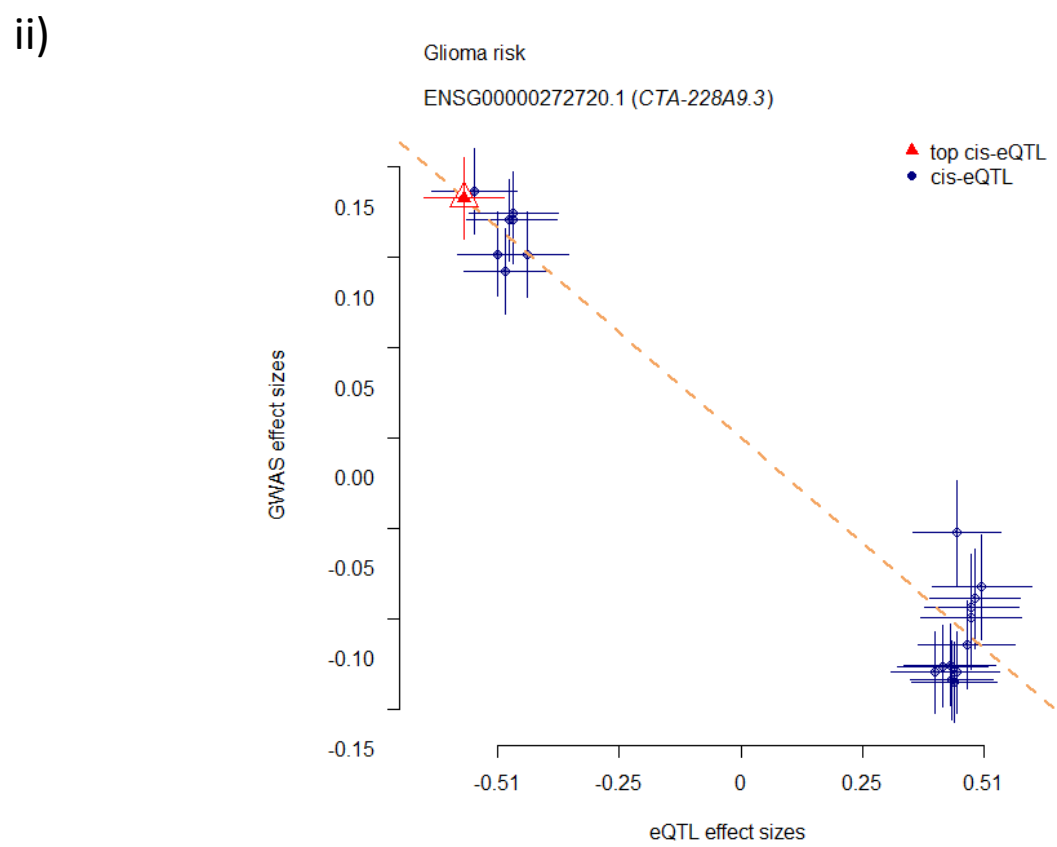
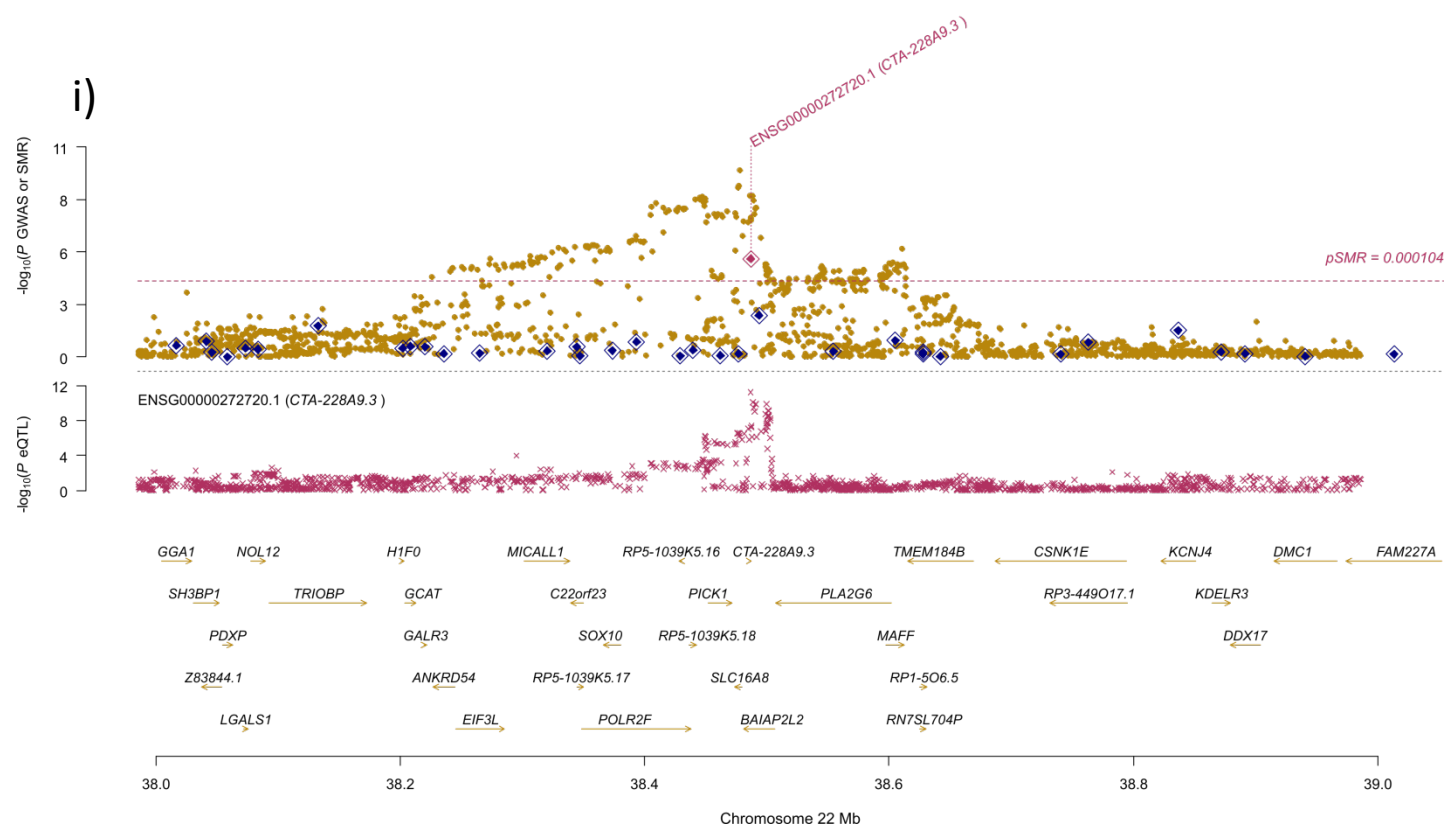
s) 16q12.1 (GBM) ENSG00000155393.8 (*HEATR3*) Brain Hippocampus



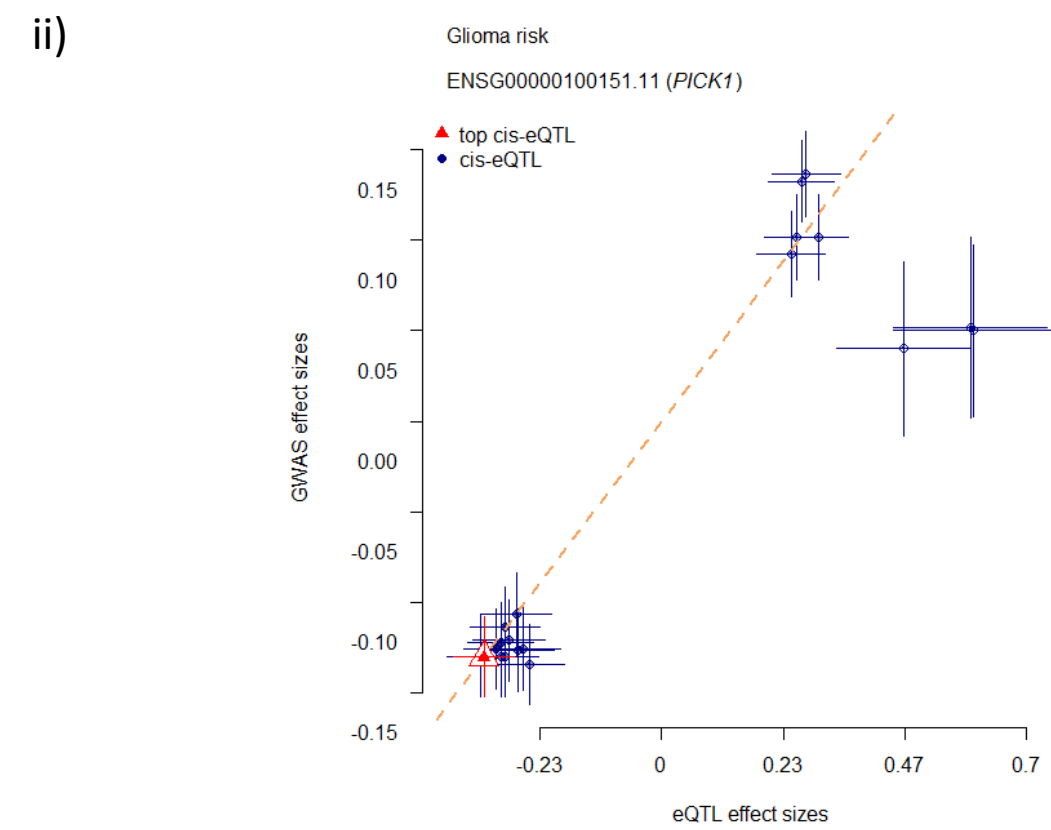
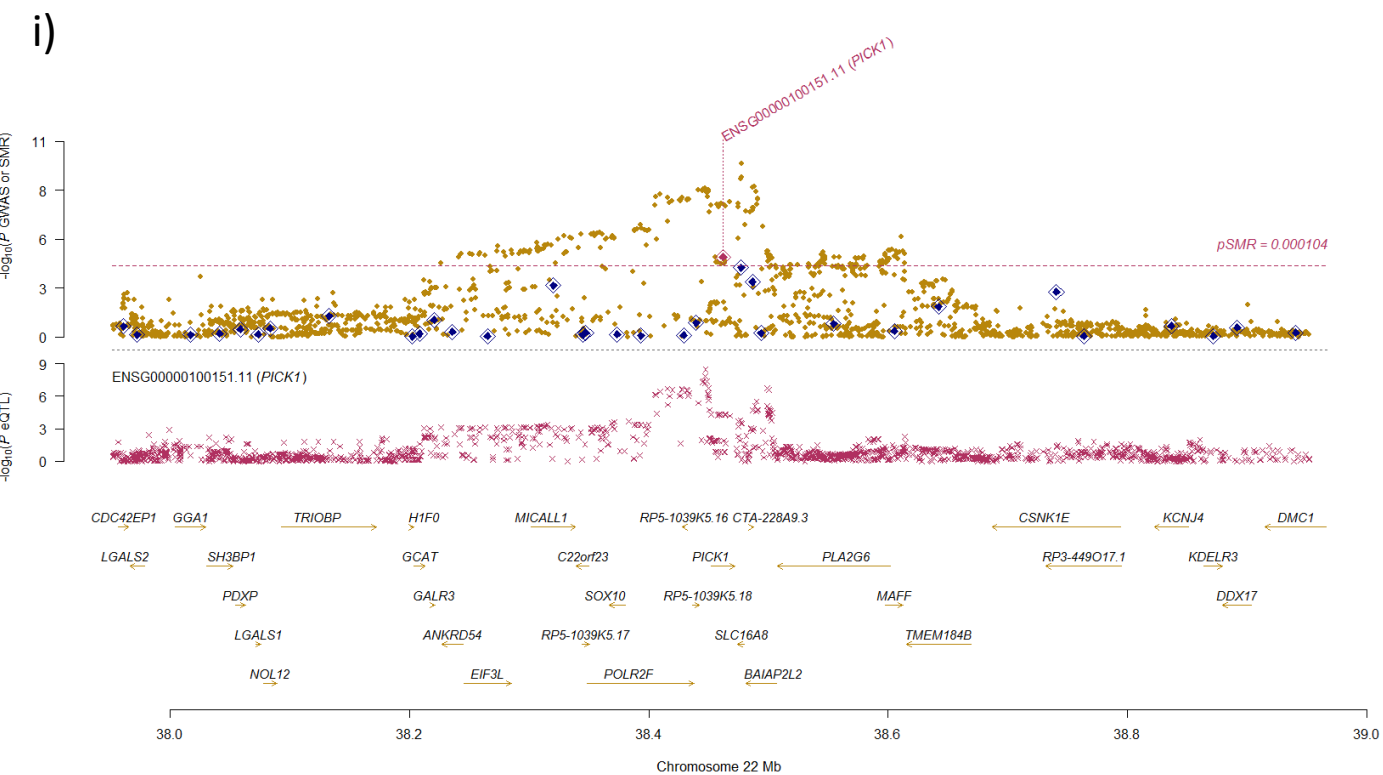
t) 16q12.1 (GBM) ENSG00000155393.8 (*HEATR3*) Brain Hypothalamus



u) 22q13.1 (GBM) ENSG00000272720.1 (CTA-228A9.3) Brain Cerebellum



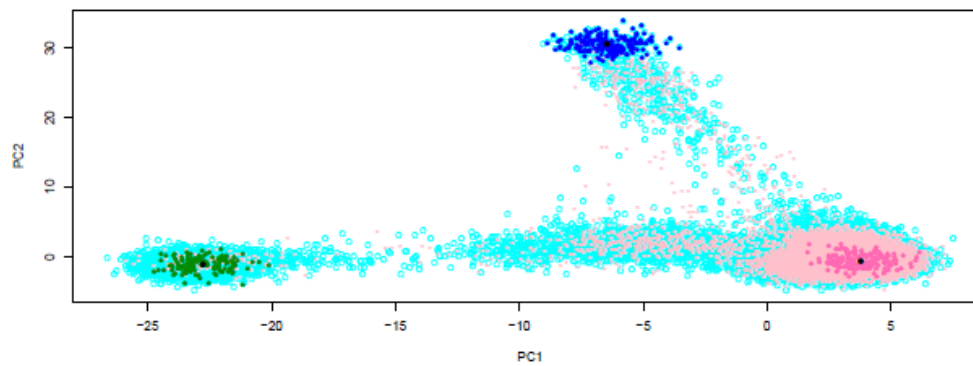
v) 22q13.1 (GBM) ENSG00000100151.11 (*PICK1*) Brain Hippocampus



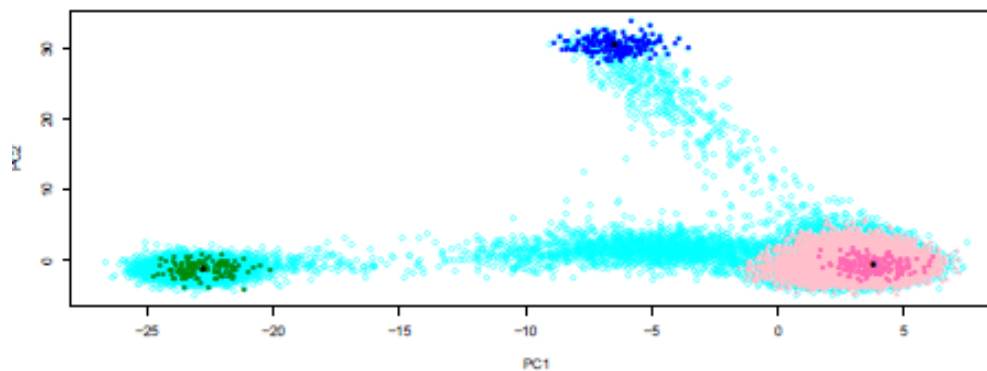
Supplementary Figure 5: PCA plots of the GWAS datasets

(a) GICC

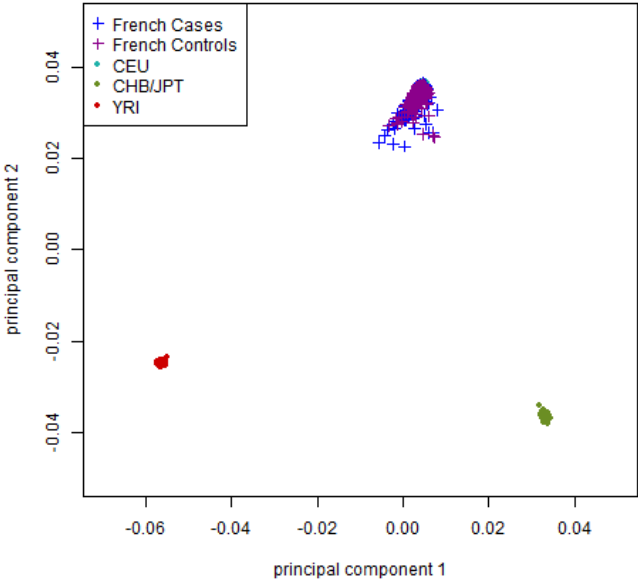
GAMEON ancestry informative marker analysis for non European ancestry assignment – ALL DATA



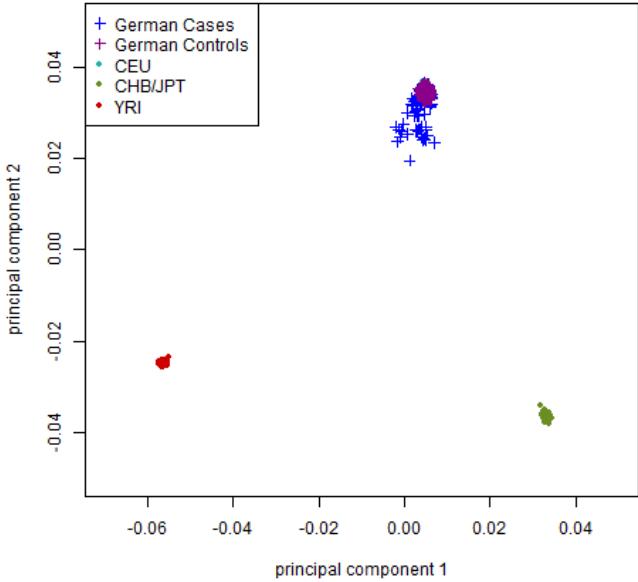
GAMEON ancestry informative marker analysis for non European ancestry assignment – individuals with <0.80 European (CEU) ancestry removed



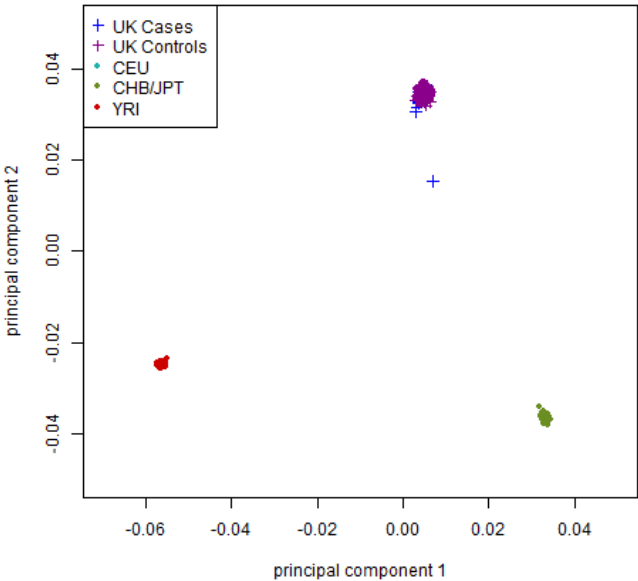
(b) French-GWAS



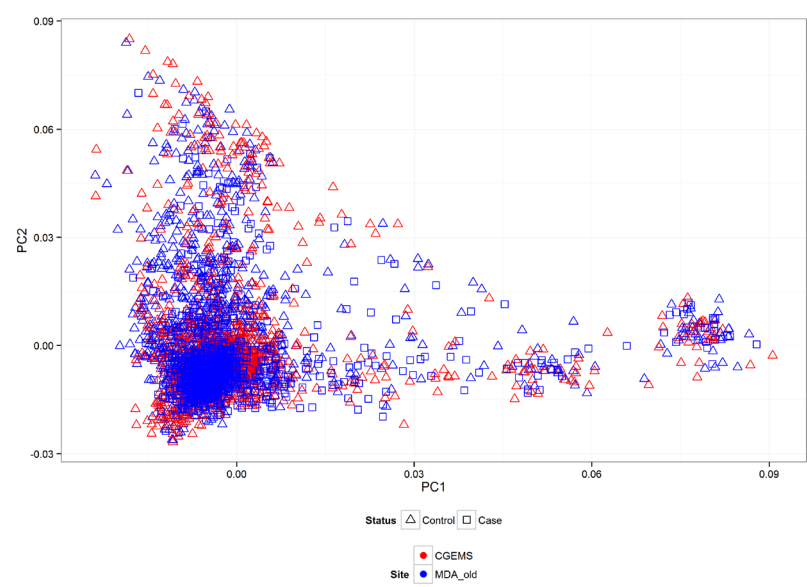
c) German-GWAS



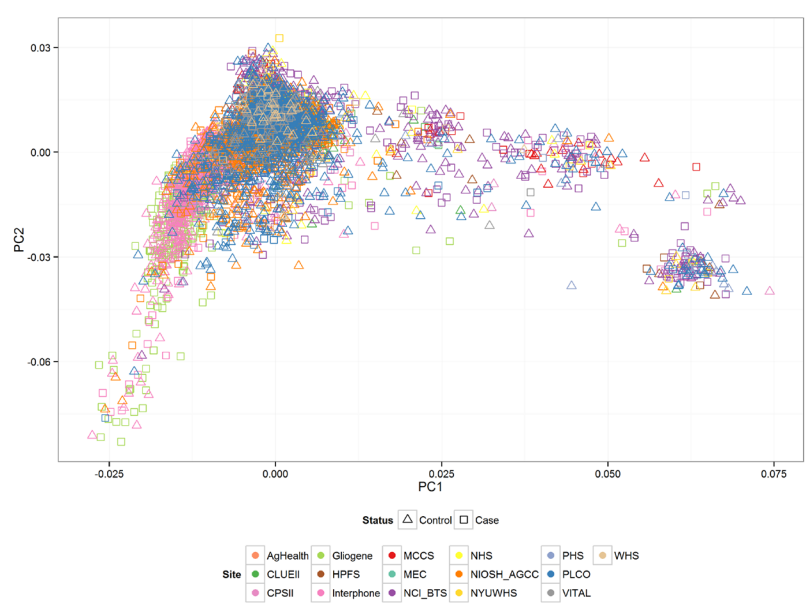
(d) UK-GWAS



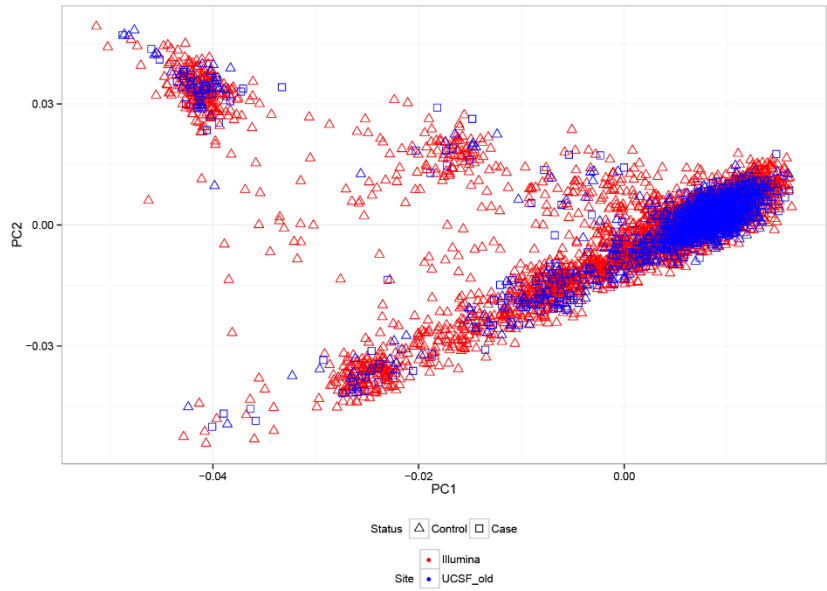
(e) MDA-GWAS



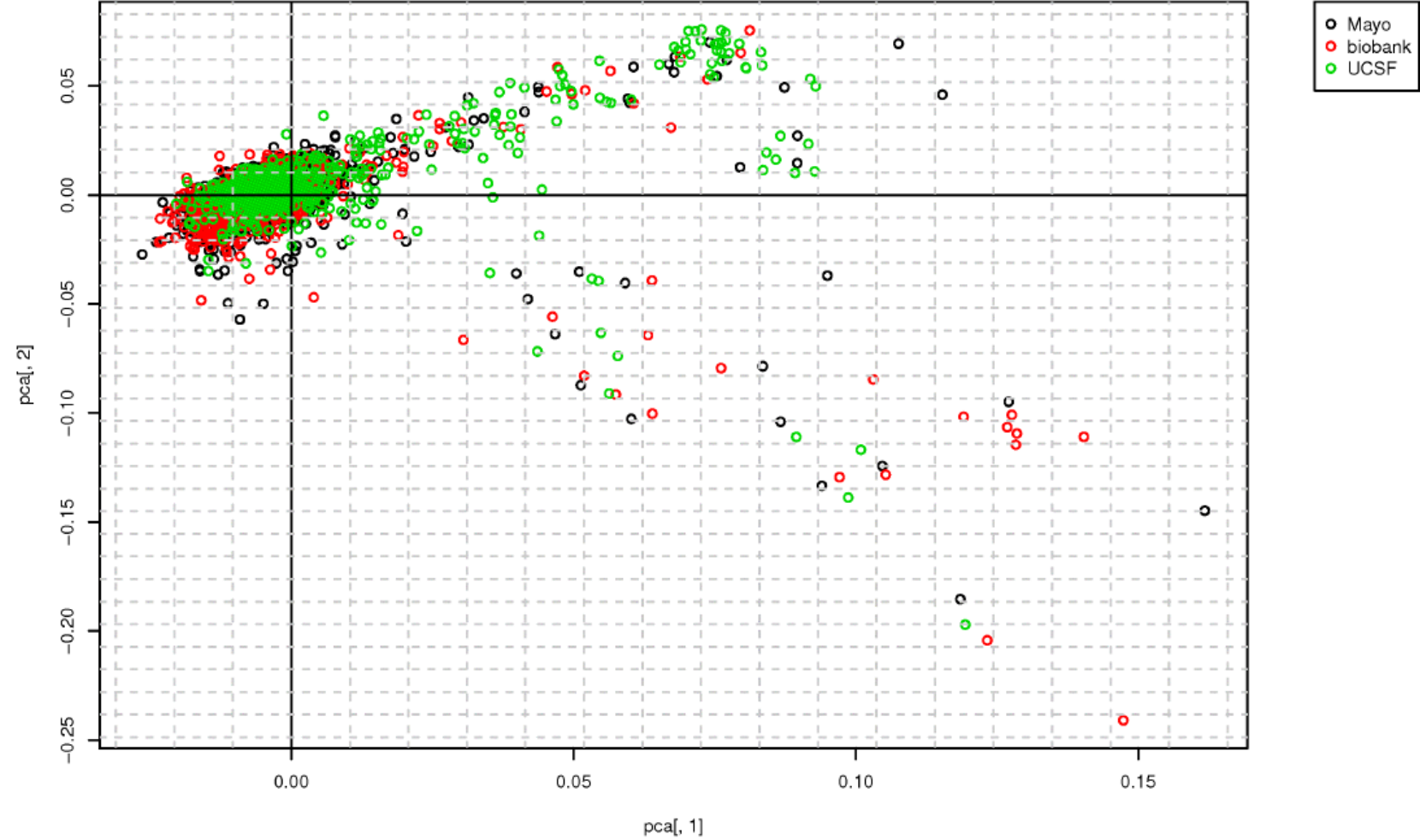
(f) GliomaScan GWAS



(g) SAFGS GWAS



(h) Mayo/UCSF



	All Glioma						GBM			Non-GBM		
	Pre-QC			Post QC			Post QC			Post QC		
	Total	Cases	Controls	Total	Cases	Controls	Total	Cases	Controls	Total	Cases	Controls
Baylor College of Medicine	40	40	0	11	11	0	6	6	0	5	5	0
Brigham and Women's Hospital	247	225	22	215	193	22	123	101	22	98	76	22
Columbia	215	64	151	166	40	126	150	24	126	141	15	126
Case Western Reserve University	74	60	14	67	56	11	44	33	11	34	23	11
Denmark	1,054	522	532	1,008	496	512	811	299	512	706	194	512
Duke	876	622	254	782	578	204	627	423	204	338	134	204
Mayo	833	376	457	803	358	445	639	194	445	604	159	445
MD Anderson	1,783	1,505	278	1,140	921	219	571	352	219	774	555	219
Memorial Sloan Kettering	652	283	369	531	239	292	416	124	292	396	104	292
North Shore	306	133	173	264	123	141	217	76	141	187	46	141
Sweden	1,400	476	924	1,356	465	891	1,162	270	891	1,079	188	891
University of California, San Francisco	673	333	340	506	277	229	381	152	229	350	121	229
UK	914	798	116	874	766	108	491	383	108	366	258	108
University of Southern California	297	98	199	135	49	86	115	29	86	105	19	86
GICC	9,364	5,535	3,829	7,858	4,572	3,286	5,754	2,466	3,286	5,183	1,897	3,286

* Israeli samples and whole genome amplified samples were excluded at the initial QC regarding DNA quality control.

Supplementary Table 1: Summary characteristics of the GICC sub-studies.

Supplementary Table 2: Details of studies and SNPs imputed

Study	Final sample numbers		Imputed SNPs
	Cases (GBM/non-GBM)	Controls	
UK-GWAS	631 (270/361)	2,699	8,954,681
French-GWAS	1,423 (430/993)	1,190	9,113,681
German-GWAS	846 (431/415)	1,310	9,012,806
MDA-GWAS	1,175 (652/523)	2,236	9,043,003
SFAGS	677 (511/166)	3,940	10,679,291
GliomaScan	1,653 (903/472)	2,725	9,161,499
GICC	4,572 (2,468/1,897)	3,286	10,783,269
UCSF/Mayo	1,519 (526/992)	804	6,915,238 ^a

	SNP numbers		
	All glioma	GBM	Non-GBM
Meta-analysis			
All SNPs	6,887,412	6,790,270	6,769,856

Successfully imputed SNPs in each discovery series GWAS were those with INFO > 0.4, case and control MAF > 0.01, P_{HWE} in controls > 1×10^{-8} . For the meta-analysis we considered all SNPs meeting the above criteria in all eight studies as well as having heterogeneity $I^2 < 75$ in all/GBM/non-GBM glioma. ^a For the UCSF/Mayo study an imputation threshold of > 0.8 was applied.

Supplementary Table 3: Associations for previously published glioma risk loci. Per locus SNPs were grouped according to the original GWAS discovery published. Also, shown are the combined associations for all eight GWAS data sets in the current study both for the previously published SNP and for the most strongly associated SNP within a 500kb window of the risk region (if different from original SNP). Associated odds ratio (OR) and *P*-values for each risk locus are shown. Odds ratios are with respect to the allele underlined and highlighted in bold. Risk allele frequency (RAF) from European samples from 1000 genomes project data. INFO column is the average imputation info score across all eight studies, with a score of 1.000 indicating the SNP is directly genotyped in all studies. References for original SNP discovery are also provided; note that not all the previously published SNPs were originally discovered and/or replicated via GWAS. Forest plots of associations at each locus are shown in **Supplementary Fig. 2**.

Locus	SNP	Position	LD (r^2/D')	RAF	Set	Included Studies	INFO	All glioma		GBM glioma		Non-GBM glioma	
								<i>P</i>	OR	<i>P</i>	OR	<i>P</i>	OR
3q26.2	rs1920116 (<u>G</u> /A) Published ¹	169579971	--	0.710	All	Discovery SFAGS	1.000	2.80x10 ⁻⁵	1.32 (1.16-1.51)	9.14x10 ⁻⁵	1.34 (1.16-1.56)	4.42x10 ⁻²	1.29 (1.01-1.64)
						Validation MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo		4.58x10 ⁻³	1.06 (1.02-1.11)	7.61x10 ⁻³	1.07 (1.02-1.13)	1.14x10 ⁻¹	1.04 (0.99-1.10)
						MDA-GWAS		1.79x10 ⁻¹	1.08 (0.97-1.21)	1.79x10 ⁻¹	1.10 (0.96-1.26)	4.07x10 ⁻¹	1.07 (0.92-1.24)
						UK-GWAS		8.67x10 ⁻¹	1.01 (0.88-1.16)	4.95x10 ⁻¹	1.07 (0.88-1.31)	7.28x10 ⁻¹	0.97 (0.82-1.15)
						French-GWAS		3.93x10 ⁻¹	1.06 (0.93-1.20)	7.01x10 ⁻¹	0.97 (0.81-1.16)	1.81x10 ⁻¹	1.10 (0.96-1.26)
						German-GWAS		2.79x10 ⁻¹	1.08 (0.94-1.24)	2.65x10 ⁻¹	1.11 (0.93-1.32)	5.74x10 ⁻¹	1.05 (0.88-1.25)
						GliomaScan		3.52x10 ⁻⁴	1.19 (1.08-1.32)	1.31x10 ⁻³	1.22 (1.08-1.37)	1.04x10 ⁻¹	1.14 (0.97-1.33)
						GICC		7.02x10 ⁻¹	1.01 (0.94-1.09)	8.45x10 ⁻¹	1.01 (0.93-1.09)	3.49x10 ⁻¹	1.04 (0.95-1.14)
						UCSF-Mayo		8.63x10 ⁻¹	0.99 (0.85-1.15)	2.72x10 ⁻¹	1.11 (0.92-1.34)	1.79x10 ⁻¹	0.88 (0.74-1.06)
						SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo		7.36x10 ⁻⁵	1.08 (1.04-1.13)	1.46x10 ⁻⁴	1.10 (1.05-1.15)	4.90x10 ⁻²	1.05 (1.00-1.11)
3q26.2	rs3772190 (<u>G</u> /A) This study	169500487	0.54/0.80	0.757	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	>0.999	2.25x10 ⁻⁶	1.11 (1.06-1.15)	2.68x10 ⁻⁵	1.11 (1.06-1.17)	1.20x10 ⁻²	1.07 (1.02-1.13)
5p15.33	rs2736100 (<u>C</u> /A) Published ^{2,3}	1286516	--	0.499	All	Discovery SFAGS, MDA-GWAS, UK-GWAS, SFAGS	1.000	2.51x10 ⁻¹²	1.26 (1.18-1.35)	3.57x10 ⁻¹⁶	1.40 (1.29-1.52)	8.70 x10 ⁻²	1.08 (0.99-1.19)
						MDA-GWAS		1.64x10 ⁻⁹	1.43 (1.28-1.61)	1.01x10 ⁻⁹	1.51 (1.32-1.72)	7.28x10 ⁻²	1.22 (0.98-1.52)
						UK-GWAS		3.20x10 ⁻³	1.17 (1.05-1.29)	1.24x10 ⁻⁵	1.32 (1.17-1.50)	9.75x10 ⁻¹	1.00 (0.87-1.14)
						Validation French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo		8.79x10 ⁻⁴	1.23 (1.09-1.38)	5.00x10 ⁻⁴	1.36 (1.14-1.62)	1.07x10 ⁻¹	1.13 (0.97-1.32)
						French-GWAS		8.24x10 ⁻³⁵	1.30 (1.25-1.36)	3.77x10 ⁻³⁹	1.41 (1.34-1.48)	8.82x10 ⁻¹⁰	1.18 (1.12-1.25)
						German-GWAS		2.85x10 ⁻³	1.18 (1.06-1.32)	1.32x10 ⁻⁴	1.36 (1.16-1.59)	8.37x10 ⁻²	1.11 (0.99-1.25)
						GliomaScan		2.50x10 ⁻⁵	1.31 (1.15-1.48)	1.57x10 ⁻⁶	1.47 (1.25-1.71)	1.02x10 ⁻¹	1.14 (0.97-1.34)
						GICC		2.04x10 ⁻⁹	1.31 (1.20-1.43)	1.94x10 ⁻⁹	1.40 (1.25-1.56)	8.50x10 ⁻³	1.21 (1.05-1.39)
						UCSF-Mayo		9.32x10 ⁻¹⁷	1.32 (1.24-1.41)	1.64x10 ⁻¹⁹	1.41 (1.31-1.52)	1.92x10 ⁻⁴	1.17 (1.08-1.27)
						SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo		7.71x10 ⁻⁷	1.42 (1.24-1.63)	5.06x10 ⁻⁵	1.41 (1.20-1.67)	3.96x10 ⁻⁵	1.41 (1.20-1.66)
5p15.33	rs10069690 (<u>C</u> /T) This study	1279790	0.22/-0.80	0.276	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	0.836	2.71x10 ⁻⁶⁶	1.45 (1.39-1.51)	8.33x10 ⁻⁷⁴	1.61 (1.53-1.69)	1.14x10 ⁻¹⁶	1.27 (1.20-1.34)
7p11.2	rs2252586 (<u>C</u> /T) Published ⁴	54978924		0.281	Discovery	MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS		9.52x10 ⁻⁸	1.18 (1.11-1.26)	2.01x10 ⁻⁸	1.26 (1.16-1.37)	1.96x10 ⁻³	1.13 (1.04-1.22)
						MDA-GWAS		9.23x10 ⁻²	1.01 (0.98-1.23)	6.66x10 ⁻²	1.14 (0.99-1.30)	5.93x10 ⁻¹	1.04 (0.89-1.21)

						UK-GWAS				3.36x10 ⁻²	1.16 (1.01-1.32)	5.64x10 ⁻²	1.21 (0.99-1.47)	1.88x10 ⁻¹	1.12 (0.95-1.33)
						French-GWAS				1.72x10 ⁻⁴	1.25 (1.11-1.40)	2.13x10 ⁻⁵	1.43 (1.21-1.69)	1.08x10 ⁻²	1.18 (1.04-1.34)
						German-GWAS				1.57x10 ⁻³	1.24 (1.09-1.42)	6.24x10 ⁻⁴	1.35 (1.13-1.59)	1.04x10 ⁻¹	1.16 (0.97-1.38)
					Validation	SFAGS, GliomaScan, GICC, UCSF-Mayo				1.99x10 ⁻⁷	1.14 (1.09-1.20)	2.94x10 ⁻⁸	1.18 (1.11-1.25)	2.51x10 ⁻²	1.08 (1.01-1.16)
						SFAGS				6.57x10 ⁻¹	1.03 (0.91-1.17)	2.14x10 ⁻¹	1.10 (0.95-1.26)	2.07x10 ⁻¹	0.86 (0.67-1.09)
						GliomaScan				1.14x10 ⁻²	1.13 (1.03-1.25)	1.35x10 ⁻²	1.16 (1.03-1.31)	6.47x10 ⁻¹	1.04 (0.89-1.21)
						GICC				5.20x10 ⁻⁶	1.18 (1.10-1.27)	9.84x10 ⁻⁷	1.23 (1.13-1.33)	2.44x10 ⁻²	1.11 (1.01-1.21)
						UCSF-Mayo				8.02x10 ⁻²	1.15 (0.98-1.33)	2.29x10 ⁻¹	1.12 (0.93-1.33)	7.32x10 ⁻²	1.18 (0.98-1.41)
				0.281	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo		1.000		1.38x10 ⁻¹³	1.16 (1.11-1.20)	7.89x10 ⁻¹⁵	1.20 (1.15-1.26)	1.89x10 ⁻⁴	1.10 (1.05-1.16)
7p11.2	rs75061358 (T/G) This study	54916280	0.20/0.96	0.099	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo		0.914		3.62x10 ⁻²⁷	1.42 (1.33-1.52)	4.94x10 ⁻³⁴	1.63 (1.50-1.76)	1.54x10 ⁻⁸	1.28 (1.18-1.40)
7p11.2	rs11979158 (A/G) Published ⁴	55159349	--		Discovery	MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS				7.30x10 ⁻⁷	1.22 (1.13-1.32)	1.45x10 ⁻⁷	1.32 (1.19-1.46)	1.28x10 ⁻²	1.13 (1.03-1.24)
						MDA-GWAS				4.99x10 ⁻²	1.15 (1.00-1.32)	1.50x10 ⁻²	1.23 (1.04-1.45)	7.64x10 ⁻¹	1.03 (0.86-1.23)
						UK-GWAS				3.97x10 ⁻³	1.27 (1.08-1.49)	5.87x10 ⁻²	1.25 (0.99-1.58)	1.89x10 ⁻²	1.28 (1.04-1.57)
						French-GWAS				1.75x10 ⁻²	1.22 (1.03-1.43)	1.61x10 ⁻²	1.32 (1.05-1.66)	8.44x10 ⁻²	1.17 (0.98-1.39)
						German-GWAS				4.49x10 ⁻³	1.28 (1.08-1.52)	9.63x10 ⁻⁵	1.54 (1.24-1.91)	5.21x10 ⁻¹	1.07 (0.87-1.33)
					Validation	SFAGS, GliomaScan, GICC, UCSF-Mayo				2.79x10 ⁻¹²	1.25 (1.17-1.33)	2.40x10 ⁻¹³	1.31 (1.22-1.41)	1.68x10 ⁻⁴	1.17 (1.08-1.28)
						SFAGS				6.57x10 ⁻³	1.26 (1.07-1.48)	3.28x10 ⁻³	1.32 (1.10-1.58)	6.72x10 ⁻¹	1.07 (0.79-1.44)
						GliomaScan				1.04x10 ⁻²	1.17 (1.04-1.32)	5.63x10 ⁻⁴	1.30 (1.12-1.51)	1.36x10 ⁻¹	1.16 (0.96-1.40)
						GICC				1.63x10 ⁻⁸	1.30 (1.19-1.42)	8.92x10 ⁻⁹	1.35 (1.22-1.50)	6.04x10 ⁻³	1.17 (1.04-1.30)
						UCSF-Mayo				2.80x10 ⁻²	1.22 (1.02-1.47)	1.90x10 ⁻¹	1.16 (0.93-1.43)	1.96x10 ⁻²	1.30 (1.04-1.62)
				0.831	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo		1.000		1.21x10 ⁻¹⁷	1.24 (1.18-1.30)	1.94x10 ⁻¹⁹	1.31 (1.24-1.39)	7.73x10 ⁻⁶	1.16 (1.08-1.23)
7p11.2	rs723527 (A/G) This study	55134872	0.20/0.96	0.573	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo		0.996		5.83x10 ⁻¹⁷	1.17 (1.13-1.21)	4.79x10 ⁻²³	1.25 (1.20-1.31)	8.25x10 ⁻⁴	1.08 (1.03-1.14)
8q24.21	rs55705857 (A/G) Published ^{3,5}	130645692	--		Discovery	MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS				7.56x10 ⁻³⁸	2.21 (1.96-2.50)	1.29x10 ⁻²	1.25 (1.05-1.49)	4.13x10 ⁻⁶⁷	3.84 (3.29-4.47)
						MDA-GWAS				1.81x10 ⁻¹¹	2.06 (1.67-2.54)	1.08x10 ⁻¹	1.26 (0.95-1.66)	5.92x10 ⁻²³	4.36 (3.26-5.85)
						UK-GWAS				5.49x10 ⁻¹⁰	2.34 (1.79-3.06)	7.42x10 ⁻¹	1.07 (0.72-1.59)	5.92x10 ⁻¹⁸	4.77 (3.34-6.80)
						French-GWAS				2.29x10 ⁻¹²	2.30 (1.82-2.90)	6.04x10 ⁻¹	1.12 (0.74-1.69)	9.22x10 ⁻¹⁹	3.10 (2.41-3.99)
						German-GWAS				8.28x10 ⁻⁹	2.24 (1.70-2.94)	1.92x10 ⁻²	1.57 (1.08-2.28)	1.63x10 ⁻¹³	3.90 (2.72-5.61)
					Validation	SFAGS, GliomaScan, GICC, UCSF-Mayo				1.03x10 ⁻⁴³	1.88 (1.72-2.05)	2.32x10 ⁻⁵	1.28 (1.14-1.44)	1.41x10 ⁻⁸⁴	3.15 (2.81-3.54)
						SFAGS				5.91x10 ⁻⁵	1.93 (1.40-2.66)	1.70x10 ⁻³	1.79 (1.24-2.57)	1.32x10 ⁻³	2.93 (1.52-5.65)
						GliomaScan				1.06x10 ⁻⁹	1.75 (1.46-2.09)	5.54x10 ⁻³	1.39 (1.10-1.75)	1.54x10 ⁻¹³	3.11 (2.30-4.21)
						GICC				1.99x10 ⁻²⁷	1.93 (1.71-2.17)	2.23x10 ⁻²	1.20 (1.03-1.40)	1.21x10 ⁻⁶⁰	3.26 (2.83-3.75)
						UCSF-Mayo				2.76x10 ⁻⁶	1.87 (1.44-2.43)	5.96x10 ⁻¹	1.10 (0.77-1.56)	1.16x10 ⁻¹¹	2.78 (2.07-3.74)
				0.057	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo		0.813		9.53x10 ⁻⁷⁹	1.99 (1.85-2.13)	9.45x10 ⁻⁷	1.27 (1.16-1.40)	7.28x10 ⁻¹⁴⁹	3.39 (3.09-3.71)
9p21.3	rs4977756 (G/A) Published ^{2,3}	22068652	--		Discovery	SFAGS, MDA-GWAS, UK-GWAS				5.19x10 ⁻¹²	1.26 (1.18-1.35)	2.93x10 ⁻¹²	1.34 (1.23-1.45)	1.19x10 ⁻³	1.17 (1.06-1.29)
						SFAGS				7.37x10 ⁻⁶	1.32 (1.17-1.49)	6.84x10 ⁻⁶	1.37 (1.19-1.57)	9.79x10 ⁻²	1.21 (0.97-1.52)
						MDA-GWAS				1.17x10 ⁻⁵	1.26 (1.13-1.39)	9.66x10 ⁻⁵	1.29 (1.13-1.46)	4.25x10 ⁻³	1.23 (1.07-1.41)
						UK-GWAS				2.31x10 ⁻³	1.21 (1.07-1.37)	1.75x10 ⁻⁴	1.41 (1.18-1.68)	3.09x10 ⁻¹	1.08 (0.93-1.27)

9p21.3	rs634537 (T/G) This study	22032152	0.77/-0.92	0.400	Validation	French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	1.000	3.31x10 ⁻³¹	1.29 (1.23-1.34)	1.90x10 ⁻²⁹	1.34 (1.28-1.42)	3.95x10 ⁻¹²	1.21 (1.15-1.28)
					<i>French-GWAS</i>	8.01x10 ⁻⁷		1.32 (1.18-1.48)	2.63x10 ⁻⁴	1.35 (1.15-1.58)	9.00x10 ⁻⁶	1.32 (1.17-1.49)	
					<i>German-GWAS</i>	1.83x10 ⁻⁴		1.27 (1.12-1.45)	9.59x10 ⁻²	1.15 (0.98-1.35)	3.10x10 ⁻⁵	1.41 (1.20-1.66)	
					<i>GliomaScan</i>	5.08x10 ⁻⁷		1.25 (1.15-1.37)	8.11x10 ⁻⁹	1.38 (1.23-1.53)	2.05x10 ⁻¹	1.10 (0.95-1.26)	
					<i>GICC</i>	2.24x10 ⁻¹⁶		1.31 (1.23-1.40)	9.40x10 ⁻¹⁷	1.37 (1.27-1.48)	2.04x10 ⁻⁵	1.19 (1.10-1.29)	
					<i>UCSF-Mayo</i>	1.30x10 ⁻²		1.19 (1.04-1.37)	3.66x10 ⁻⁴	1.36 (1.15-1.61)	3.92x10 ⁻¹	1.07 (0.91-1.27)	
					SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	1.46x10 ⁻⁴¹		1.28 (1.23-1.32)	4.24x10 ⁻⁴⁰	1.34 (1.29-1.40)	2.28x10 ⁻¹⁴	1.20 (1.15-1.26)	
					SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	1.24x10 ⁻⁴⁵		1.30 (1.25-1.34)	7.23x10 ⁻⁴⁵	1.37 (1.31-1.43)	1.05x10 ⁻¹⁵	1.21 (1.16-1.27)	
10q25.2	rs11196067 (A/T) Published ⁶	114469065	--	0.579	Discovery	MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS	0.985	2.53x10 ⁻⁷	1.16 (1.10-1.23)	7.69x10 ⁻²	1.07 (0.99-1.16)	3.50x10 ⁻¹⁰	1.26 (1.17-1.35)
					<i>MDA-GWAS</i>	4.37x10 ⁻¹		1.05 (0.92-1.20)	8.79x10 ⁻¹	0.99 (0.84-1.16)	1.45x10 ⁻¹	1.13 (0.96-1.34)	
					<i>UK-GWAS</i>	8.74x10 ⁻¹		0.99 (0.91-1.09)	9.89x10 ⁻¹	1.00 (0.89-1.12)	9.19x10 ⁻¹	1.01 (0.87-1.17)	
					<i>French-GWAS</i>	3.11x10 ⁻⁵		1.26 (1.13-1.41)	1.97x10 ⁻¹	1.11 (0.95-1.30)	2.19x10 ⁻⁶	1.34 (1.19-1.51)	
					<i>German-GWAS</i>	1.43x10 ⁻²		1.09 (1.02-1.16)	2.52x10 ⁻¹	1.05 (0.97-1.13)	1.25x10 ⁻³	1.15 (1.06-1.25)	
					Validation	SFAGS, GliomaScan, GICC, UCSF-Mayo		2.60x10 ⁻¹	1.03 (0.98-1.08)	7.06x10 ⁻¹	1.01 (0.96-1.07)	2.14x10 ⁻²	1.08 (1.01-1.15)
						<i>SFAGS</i>		8.73x10 ⁻¹	0.99 (0.86-1.14)	9.67x10 ⁻¹	1.00 (0.85-1.18)	8.82x10 ⁻¹	0.99 (0.84-1.17)
						<i>GliomaScan</i>		2.34x10 ⁻¹	0.93 (0.82-1.05)	2.49x10 ⁻¹	0.92 (0.80-1.06)	5.86x10 ⁻¹	0.94 (0.74-1.18)
						<i>GICC</i>		1.02x10 ⁻²	1.15 (1.03-1.27)	1.80x10 ⁻¹	1.09 (0.96-1.24)	1.44x10 ⁻³	1.26 (1.09-1.45)
						<i>UCSF-Mayo</i>		1.05x10 ⁻²	1.18 (1.04-1.33)	3.32x10 ⁻¹	1.09 (0.91-1.31)	7.01x10 ⁻³	1.24 (1.06-1.46)
						SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo		3.79x10 ⁻⁵	1.08 (1.04-1.12)	0.182	1.03 (0.99-1.08)	3.53x10 ⁻⁹	1.15 (1.10-1.21)
10q25.2	rs11599775 (G/A) This study	114459697	0.89/1.00	0.620	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	0.967	4.34x10 ⁻⁵	1.08 (1.04-1.12)	2.99x10 ⁻¹	1.02 (0.98-1.07)	3.44x10 ⁻⁹	1.16 (1.10-1.22)
11q23.2	rs648044 (A/G) Published ³	114030799	--	0.390	Discovery	MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS	0.897	2.83x10 ⁻²	1.08 (1.01-1.15)	3.69x10 ⁻¹	0.96 (0.89-1.05)	1.25x10 ⁻⁷	1.23 (1.14-1.33)
					<i>MDA-GWAS</i>	4.19x10 ⁻¹		0.95 (0.82-1.08)	4.19x10 ⁻¹	0.95 (0.82-1.08)	1.45x10 ⁻²	1.21 (1.04-1.40)	
					<i>UK-GWAS</i>	8.46x10 ⁻¹		1.01 (0.89-1.16)	4.19x10 ⁻²	0.82 (0.67-0.99)	4.70x10 ⁻²	1.19 (1.00-1.40)	
					<i>French-GWAS</i>	5.18x10 ⁻³		1.18 (1.05-1.33)	8.70x10 ⁻¹	1.01 (0.85-1.20)	3.62x10 ⁻⁴	1.27 (1.11-1.44)	
					<i>German-GWAS</i>	4.32x10 ⁻²		1.16 (1.00-1.34)	3.89x10 ⁻¹	1.08 (0.90-1.30)	1.63x10 ⁻²	1.25 (1.04-1.50)	
					Validation	SFAGS, GliomaScan, GICC, UCSF-Mayo		4.44x10 ⁻²	1.05 (1.00-1.10)	6.22x10 ⁻¹	0.99 (0.93-1.04)	4.42x10 ⁻⁶	1.16 (1.09-1.24)
						<i>SFAGS</i>		7.81x10 ⁻¹	1.02 (0.89-1.16)	3.37x10 ⁻¹	0.93 (0.80-1.08)	2.09x10 ⁻²	1.35 (1.05-1.75)
						<i>GliomaScan</i>		7.22x10 ⁻¹	0.98 (0.89-1.08)	5.79x10 ⁻¹	0.97 (0.86-1.09)	7.05x10 ⁻¹	0.97 (0.83-1.13)
						<i>GICC</i>		4.91x10 ⁻²	1.07 (1.00-1.14)	9.87x10 ⁻¹	1.00 (0.93-1.08)	1.05x10 ⁻⁴	1.18 (1.08-1.28)
						<i>UCSF-Mayo</i>		4.44x10 ⁻²	1.16 (1.00-1.34)	7.16x10 ⁻¹	1.03 (0.87-1.23)	3.01x10 ⁻³	1.29 (1.09-1.53)
						SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo		3.55x10 ⁻³	1.06 (1.02-1.10)	3.63 x10 ⁻¹	0.98 (0.93-1.03)	4.66x10 ⁻¹²	1.19 (1.13-1.25)
11q23.3	rs498872 (A/G) Published ⁶	118477367	--		Discovery	MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS		1.84x10 ⁻⁷	1.19 (1.11-1.27)	8.07x10 ⁻²	1.08 (0.99-1.17)	3.39x10 ⁻¹⁷	1.38 (1.28-1.48)
					<i>MDA-GWAS</i>		1.14x10 ⁻¹	1.12 (0.97-1.28)	1.14x10 ⁻¹	1.12 (0.97-1.28)	7.70x10 ⁻⁹	1.54 (1.33-1.78)	
					<i>UK-GWAS</i>		2.28x10 ⁻²	1.17 (1.02-1.33)	8.57x10 ⁻²	1.18 (0.98-1.43)	9.21x10 ⁻²	1.16 (0.98-1.37)	

						French-GWAS German-GWAS			2.61x10 ⁻⁴ 1.24 (1.10-1.38) 5.78x10 ⁻³ 1.21 (1.06-1.39)	6.95x10 ⁻¹ 0.97 (0.82-1.14) 5.80x10 ⁻¹ 1.05 (0.88-1.25)	5.77x10 ⁻⁷ 1.37 (1.21-1.55) 4.77x10 ⁻⁵ 1.44 (1.21-1.71)
					Validation	SFAGS, GliomaScan, GICC, UCSF-Mayo			1.41x10 ⁻⁵ 1.11 (1.06-1.17) 1.91x10 ⁻¹ 1.09 (0.96-1.23)	4.43x10 ⁻¹ 0.98 (0.92-1.04) 4.80x10 ⁻¹ 0.95 (0.82-1.10)	2.33x10 ⁻¹⁷ 1.32 (1.24-1.41) 2.61x10 ⁻⁵ 1.66 (1.31-2.09)
						SFAGS GliomaScan GICC UCSF-Mayo			7.52x10 ⁻² 1.09 (0.99-1.20) 1.86x10 ⁻⁴ 1.14 (1.06-1.22) 3.16x10 ⁻¹ 1.08 (0.93-1.24)	1.91x10 ⁻¹ 0.92 (0.82-1.04) 7.74x10 ⁻¹ 1.01 (0.93-1.10) 8.43x10 ⁻¹ 0.98 (0.82-1.17)	4.35x10 ⁻⁵ 1.37 (1.18-1.59) 2.32x10 ⁻¹⁰ 1.31 (1.21-1.43) 7.56x10 ⁻² 1.17 (0.98-1.38)
				0.307	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	1.000		4.09x10 ⁻¹¹ 1.14 (1.10-1.18)	7.15 x10 ⁻¹ 1.01 (0.96-1.06)	8.46x10 ⁻³³ 1.35 (1.28-1.41)
11q23.3	rs12803321 (G/C) This study	118480115	0.24/0.99	0.643	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	0.976		9.93x10 ⁻¹⁶ 1.17 (1.27-1.22)	7.69x10 ⁻¹ 1.01 (0.96-1.05)	6.33x10 ⁻⁴³ 1.42 (1.35-1.49)
12q21.2	rs12230172 (A/G) Published ⁶	76242675	--		Discovery	MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS			4.38x10 ⁻³ 1.09 (1.03-1.15)	7.69x10 ⁻¹ 0.99 (0.92-1.07)	7.25x10 ⁻⁶ 1.17 (1.09-1.26)
						MDA-GWAS UK-GWAS French-GWAS German-GWAS			3.14x10 ⁻¹ 1.05 (0.95-1.17) 4.74x10 ⁻¹ 1.05 (0.93-1.18) 4.52x10 ⁻² 1.12 (1.00-1.24) 4.31x10 ⁻² 1.14 (1.00-1.30)	6.40x10 ⁻¹ 0.97 (0.86-1.10) 8.07x10 ⁻¹ 1.02 (0.86-1.22) 6.66x10 ⁻¹ 0.97 (0.83-1.13) 8.42x10 ⁻¹ 1.02 (0.87-1.19)	2.86x10 ⁻² 1.17 (1.02-1.34) 4.38x10 ⁻¹ 1.06 (0.91-1.24) 4.12x10 ⁻³ 1.19 (1.06-1.34) 2.17x10 ⁻³ 1.29 (1.10-1.52)
					Validation	SFAGS, GliomaScan, GICC, UCSF-Mayo			3.55x10 ⁻¹ 1.02 (0.98-1.07) 1.06x10 ⁻¹ 0.91 (0.81-1.02)	5.89x10 ⁻¹ 0.99 (0.93-1.04) 1.57x10 ⁻¹ 0.91 (0.80-1.04)	3.65x10 ⁻² 1.07 (1.00-1.14) 3.45x10 ⁻¹ 0.90 (0.72-1.12)
						SFAGS GliomaScan GICC UCSF-Mayo			3.65x10 ⁻² 1.10 (1.01-1.20) 9.60x10 ⁻¹ 1.00 (0.94-1.07) 1.84x10 ⁻¹ 1.10 (0.96-1.26)	2.16x10 ⁻² 1.14 (1.02-1.27) 7.32x10 ⁻² 0.93 (0.87-1.01) 5.77x10 ⁻¹ 1.05 (0.89-1.23)	3.25x10 ⁻¹ 1.07 (0.93-1.24) 1.18x10 ⁻¹ 1.07 (0.98-1.16) 5.57x10 ⁻² 1.17 (1.00-1.38)
				0.543	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	0.999		0.012 1.05 (1.01-1.08)	5.41 x10 ⁻¹ 0.99 (0.94-1.03)	5.50x10 ⁻⁶ 1.11 (1.06-1.17)
12q21.2	rs1275600 (T/A) This study	76263551	0.40/-0.72	0.595	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	0.994		2.67x10 ⁻⁴ 1.07 (1.03-1.11)	8.62x10 ⁻¹ 1.00 (0.96-1.05)	3.72x10 ⁻⁹ 1.16 (1.10-1.21)
12q23.33	rs3851634 (T/C) Published ⁶	106812902	--		Discovery	MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS			8.52x10 ⁻⁶ 1.15 (1.08-1.23)	1.02x10 ⁻⁷ 1.25 (1.15-1.36)	7.45x10 ⁻² 1.07 (0.99-1.16)
						MDA-GWAS UK-GWAS French-GWAS German-GWAS			6.14x10 ⁻² 1.12 (0.99-1.26) 7.36x10 ⁻¹ 1.03 (0.88-1.19) 3.29x10 ⁻¹ 0.96 (0.90-1.04) 4.02x10 ⁻⁴ 1.23 (1.10-1.38)	2.37x10 ⁻² 1.22 (1.03-1.45) 7.96x10 ⁻¹ 1.02 (0.85-1.23) 9.40x10 ⁻¹ 1.00 (0.92-1.09) 4.88x10 ⁻⁴ 1.28 (1.12-1.48)	2.46x10 ⁻¹ 1.08 (0.95-1.23) 4.88x10 ⁻¹ 1.06 (0.89-1.27) 1.23x10 ⁻¹ 0.93 (0.85-1.02) 6.92x10 ⁻² 1.15 (0.99-1.34)
					Validation	SFAGS, GliomaScan, GICC, UCSF-Mayo			8.91x10 ⁻¹ 1.00 (0.95-1.06) 5.10x10 ⁻² 1.14 (1.00-1.31) 1.77x10 ⁻¹ 1.10 (0.96-1.27)	6.24x10 ⁻¹ 1.01 (0.96-1.08) 1.03x10 ⁻³ 1.38 (1.14-1.67) 1.24x10 ⁻¹ 1.15 (0.96-1.37)	5.15x10 ⁻¹ 0.98 (0.91-1.05) 9.02x10 ⁻¹ 0.99 (0.83-1.17) 5.85x10 ⁻¹ 1.05 (0.88-1.26)
						SFAGS GliomaScan GICC UCSF-Mayo			8.14x10 ⁻¹ 1.01 (0.92-1.12) 1.25x10 ⁻¹ 1.11 (0.97-1.26) 3.96x10 ⁻³ 1.06 (1.02-1.10)	8.70x10 ⁻¹ 0.99 (0.88-1.12) 2.73x10 ⁻¹ 1.09 (0.94-1.26) 5.41x10 ⁻⁴ 1.09 (1.04-1.14)	7.68x10 ⁻¹ 0.98 (0.84-1.14) 1.61x10 ⁻¹ 1.19 (0.93-1.53) 0.492 1.02 (0.97-1.07)
				0.702	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	0.998				
12q23.33	rs12227783 (A/T) This study	107041782	0.03/0.32	0.851	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	0.979		5.86x10 ⁻⁵ 1.12 (1.06-1.18)	1.60x10 ⁻⁵ 1.16 (1.08-1.24)	5.80x10 ⁻² 1.07 (1.00-1.15)
15q24.2	rs1801591 (G/A)	76578762			Discovery	MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS			9.53x10 ⁻⁵ 1.21 (1.1-1.34)	3.19x10 ⁻¹ 1.07 (0.94-1.22)	2.88x10 ⁻⁷ 1.37 (1.22-1.55)

	Published ⁶					MDA-GWAS UK-GWAS French-GWAS German-GWAS		3.74x10 ⁻² 1.20 (1.01-1.43) 4.62x10 ⁻¹ 1.08 (0.88-1.33) 4.35x10 ⁻³ 1.33 (1.09-1.61) 3.71x10 ⁻² 1.25 (1.01-1.53)	9.05x10 ⁻¹ 0.99 (0.79-1.23) 8.66x10 ⁻¹ 0.97 (0.72-1.31) 3.13x10 ⁻¹ 1.16 (0.87-1.56) 1.67x10 ⁻¹ 1.20 (0.93-1.56)	2.20x10 ⁻⁴ 1.55 (1.23-1.95) 2.45x10 ⁻¹ 1.17 (0.90-1.52) 1.38x10 ⁻³ 1.42 (1.14-1.75) 5.21x10 ⁻² 1.31 (1.00-1.72)
				0.088	All	SFAGS, GliomaScan, GICC, UCSF-Mayo SFAGS GliomaScan GICC UCSF-Mayo	1.000	6.76x10 ⁻⁴ 1.14 (1.06-1.23) 2.09x10 ⁻¹ 1.14 (0.93-1.41) 1.17x10 ⁻¹ 1.13 (0.97-1.31) 2.20x10 ⁻² 1.14 (1.02-1.27) 1.15x10 ⁻¹ 1.20 (0.96-1.51) 3.56x10 ⁻⁷ 1.17 (1.10-1.24)	6.47x10 ⁻¹ 1.02 (0.93-1.12) 5.05x10 ⁻¹ 1.08 (0.86-1.37) 5.68x10 ⁻¹ 0.95 (0.78-1.14) 8.86x10 ⁻¹ 1.01 (0.89-1.15) 2.59x10 ⁻¹ 1.17 (0.89-1.54) 3.43 x10 ⁻¹ 1.04 (0.96-1.12)	3.87x10 ⁻⁷ 1.31 (1.18-1.45) 1.18x10 ⁻¹ 1.36 (0.92-2.01) 1.45x10 ⁻² 1.35 (1.06-1.72) 2.12x10 ⁻⁴ 1.29 (1.13-1.47) 5.22x10 ⁻² 1.30 (1.00-1.69) 6.36x10 ⁻¹³ 1.33 (1.23-1.44)
15q24.2	rs77633900 (G/C) This study	76538459	0.70/0.85	0.086	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	0.993	1.48x10 ⁻⁷ 1.18 (1.11-1.25)	2.58x10 ⁻¹ 1.04 (0.97-1.13)	1.60x10 ⁻¹³ 1.35 (1.25-1.46)
17p13.1	rs78378222 (T/G) Published ^{7,8}	7571752	--		Discovery	MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS		2.35x10 ⁻¹⁸ 2.80 (2.22-3.52) 2.28x10 ⁻⁹ 3.47 (2.31-5.21) 6.64x10 ⁻⁸ 2.42 (1.76-3.33) 2.26x10 ⁻⁶ 3.03 (1.92-4.81) 3.47x10 ⁻² 1.68 (1.04-2.71)	7.80x10 ⁻¹² 3.25 (2.32-4.56) 1.82x10 ⁻⁷ 4.35 (2.50-7.56) 4.12x10 ⁻⁷ 2.87 (1.91-4.31) 3.23x10 ⁻⁶ 7.42 (3.19-17.24) 7.58x10 ⁻² 1.75 (0.94-3.25)	8.34x10 ⁻¹⁵ 3.29 (2.44-4.45) 1.02x10 ⁻⁶ 4.47 (2.45-8.16) 2.77x10 ⁻³ 2.37 (1.35-4.17) 1.30x10 ⁻⁵ 3.26 (1.92-5.54) 1.16x10 ⁻¹ 1.67 (0.88-3.16)
				0.013	All	SFAGS, GliomaScan, GICC, UCSF-Mayo SFAGS GliomaScan GICC UCSF-Mayo	0.922	2.46x10 ⁻²¹ 2.38 (1.99-2.84) 4.35x10 ⁻⁴ 2.67 (1.55-4.62) 6.64x10 ⁻⁸ 2.42 (1.76-3.33) 1.01x10 ⁻⁸ 2.13 (1.65-2.76) 2.54x10 ⁻⁵ 3.28 (1.89-5.69) 8.64x10 ⁻³⁸ 2.53 (2.19-2.91)	3.17x10 ⁻¹⁹ 2.45 (2.01-2.98) 2.63x10 ⁻³ 2.65 (1.40-5.01) 4.12x10 ⁻⁷ 2.87 (1.91-4.31) 1.01x10 ⁻⁸ 2.13 (1.65-2.76) 7.32x10 ⁻⁵ 3.42 (1.86-6.29) 4.82x10 ⁻²⁹ 2.63 (2.22-3.11)	2.43x10 ⁻¹⁴ 2.45 (1.94-3.08) 2.16x10 ⁻² 3.41 (1.20-9.71) 2.77x10 ⁻³ 2.37 (1.35-4.17) 8.41x10 ⁻⁹ 2.31 (1.74-3.08) 6.47x10 ⁻⁴ 2.95 (1.59-5.50) 4.70x10 ⁻²⁷ 2.73 (2.27-3.28)
20q13.33	rs6010620 (A/G) Published ^{2,3}	62309839	--		Discovery	SFAGS, MDA-GWAS, UK-GWAS		7.02x10 ⁻¹⁴ 1.35 (1.25-1.46) 8.47x10 ⁻⁸ 1.48 (1.28-1.71) 1.27x10 ⁻³ 1.22 (1.08-1.38) 3.87x10 ⁻⁶ 1.41 (1.22-1.62)	1.66x10 ⁻¹⁴ 1.46 (1.33-1.61) 6.53x10 ⁻⁸ 1.56 (1.33-1.83) 4.99x10 ⁻⁴ 1.30 (1.12-1.52) 3.43x10 ⁻⁶ 1.64 (1.33-2.02)	2.36x10 ⁻³ 1.19 (1.06-1.32) 9.92x10 ⁻² 1.25 (0.96-1.63) 1.84x10 ⁻¹ 1.12 (0.95-1.31) 1.67x10 ⁻² 1.25 (1.04-1.49)
				0.794	All	French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo French-GWAS German-GWAS GliomaScan GICC UCSF-Mayo	1.000	5.03x10 ⁻²⁸ 1.34 (1.27-1.41) 1.78x10 ⁻² 1.19 (1.03-1.36) 6.34x10 ⁻² 1.16 (0.99-1.36) 3.73x10 ⁻¹¹ 1.44 (1.30-1.61) 2.37x10 ⁻¹⁴ 1.37 (1.26-1.49) 1.73x10 ⁻⁵ 1.44 (1.22-1.70) 2.81x10 ⁻⁴⁰ 1.34 (1.29-1.40)	4.02x10 ⁻³¹ 1.46 (1.37-1.55) 1.26x10 ⁻⁴ 1.48 (1.21-1.81) 5.55x10 ⁻³ 1.32 (1.09-1.61) 9.68x10 ⁻⁹ 1.47 (1.29-1.68) 7.95x10 ⁻¹⁵ 1.44 (1.31-1.58) 4.08x10 ⁻⁶ 1.64 (1.33-2.03) 5.49x10 ⁻⁴⁴ 1.46 (1.38-1.54)	3.04x10 ⁻⁷ 1.19 (1.11-1.27) 3.62x10 ⁻¹ 1.07 (0.92-1.25) 8.48x10 ⁻¹ 1.02 (0.84-1.24) 6.09x10 ⁻⁵ 1.41 (1.19-1.67) 4.45x10 ⁻⁴ 1.19 (1.08-1.31) 2.04x10 ⁻² 1.26 (1.04-1.53) 2.60x10 ⁻⁹ 1.19 (1.12-1.25)
20q13.33	rs2297440 (T/C) This study	62312299	0.97/1.00	0.796	All	SFAGS, MDA-GWAS, UK-GWAS, French-GWAS, German-GWAS, GliomaScan, GICC, UCSF-Mayo	0.993	1.60x10 ⁻⁴² 1.36 (1.30-1.42)	3.66x10 ⁻⁴⁶ 1.48 (1.40-1.56)	6.90x10 ⁻¹⁰ 1.20 (1.13-1.26)

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3. Shete, S. *et al.* Genome-wide association study identifies five susceptibility loci for glioma. *Nat Genet* **41**, 899-904 (2009).
4. Sanson, M. *et al.* Chromosome 7p11.2 (EGFR) variation influences glioma risk. *Human molecular genetics* **20**, 2897-904 (2011).
5. Jenkins, R.B. *et al.* A low-frequency variant at 8q24.21 is strongly associated with risk of oligodendroglial tumors and astrocytomas with IDH1 or IDH2 mutation. *Nature Genetics* **44**, 1122-5 (2012).
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8. Stacey, S.N. *et al.* A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. *Nature Genetics* **43**, 1098-103 (2011).

Supplementary Table 4 – Association statistics for GBM vs non-GBM at newly reported and previously reported glioma risk SNPs.

Locus	SNP	Position	Alleles	RAF	$P_{GBM-Non-GBM}$	Odds ratio
New loci						
1p31.3	rs12752552	65229299	<u>T</u> /C	0.870	0.011	1.11 (1.02-1.21)
1q32.1	rs4252707	204508147	G/ <u>A</u>	0.220	3.09×10^{-3}	0.91 (0.85-0.97)
1q44	rs12076373	243851947	<u>G</u> /C	0.837	3.53×10^{-9}	0.80 (0.74-0.86)
2q33.3	rs7572263	209051586	<u>A</u> /G	0.756	4.75×10^{-4}	0.89 (0.84-0.95)
3p14.1	rs11706832	66502981	A/ <u>C</u>	0.456	9.45×10^{-5}	0.90 (0.85-0.95)
10q24.33	rs11598018	105661315	<u>C</u> /A	0.462	5.05×10^{-3}	0.93 (0.88-0.98)
11q14.1	rs11233250	82397014	<u>C</u> /T	0.868	1.07×10^{-8}	1.29 (1.18-1.40)
11q21	rs7107785	95747337	<u>T</u> /C	0.479	1.94×10^{-8}	0.86 (0.82-0.91)
14q12	rs10131032	33250081	<u>G</u> /A	0.916	1.29×10^{-5}	0.80 (0.73-0.89)
16p13.3	rs2562152	123896	A/ <u>T</u>	0.850	7.28×10^{-7}	1.23 (1.13-1.34)
16p13.3	rs3751667	1004554	C/ <u>T</u>	0.208	0.167	0.96 (0.90-1.02)
16q12.1	rs10852606	50128872	T/ <u>C</u>	0.713	0.039	1.07 (1.00-1.13)
22q13.1	rs2235573	38477930	<u>G</u> /A	0.507	2.08×10^{-5}	1.12 (1.06-1.18)
Known loci						
3q26.2	rs3772190	169500487	<u>G</u> /A	0.757	0.576	1.02 (0.96-1.08)
5p15.33	rs10069690	1279790	C/ <u>T</u>	0.276	2.21×10^{-14}	1.26 (1.19-1.34)
7p11.2	rs75061358	54916280	T/ <u>G</u>	0.099	8.16×10^{-7}	1.25 (1.14-1.36)
7p11.2	rs723527	55134872	<u>A</u> /G	0.573	3.17×10^{-7}	1.15 (1.09-1.22)
8q24.21	rs55705857	130645692	A/ <u>G</u>	0.057	2.49×10^{-66}	0.44 (0.40-0.49)
9p21.3	rs634537	22032152	T/ <u>G</u>	0.411	1.29×10^{-6}	1.14 (1.08-1.20)
10q25.2	rs11599775	114459697	<u>G</u> /A	0.620	1.50×10^{-3}	0.91 (0.87-0.97)
11q23.2	rs648044	114030799	<u>A</u> /G	0.390	4.42×10^{-10}	0.84 (0.79-0.89)
11q23.3	rs12803321	118480115	<u>G</u> /C	0.643	1.78×10^{-28}	0.72 (0.68-0.77)
12q21.2	rs1275600	76263551	<u>T</u> /A	0.595	1.48×10^{-8}	0.85 (0.81-0.90)
12q23.33	rs12227783	107041782	<u>A</u> /T	0.851	0.129	0.94 (0.86-1.02)
15q24.2	rs77633900	76538459	G/ <u>C</u>	0.086	3.04×10^{-7}	0.79 (0.73-0.87)
17p13.1	rs78378222	7571752	T/ <u>G</u>	0.013	0.962	1.00 (0.85-1.17)
20q13.33	rs2297440	62312299	T/ <u>C</u>	0.796	1.02×10^{-8}	1.22 (1.14-1.31)

Odds ratios for GBM vs non-GBM comparisons (case-only analysis) derived with respect to the risk allele underlined and highlighted in bold. SNPs tested are the 13 new risk SNPs (as described in Table 1) and the top SNP from each of the previously reported glioma risk loci (Supplementary Table 2). Risk allele frequency (RAF) is according to European samples from 1000 genomes project. Testing 27 SNPs stipulates a multiple testing correction of $P < 1.85 \times 10^{-3}$. Highlighted in bold are P -values for SNPs showing significant GBM vs non-GBM differences in genotype frequency.

Supplementary Table 5: Genomic annotation of new glioma risk loci.

Locus	SNP	Position	r ²	D'	GERP	CADD	Gene	Annotation	RegulomeDB	FANTOM5	Super-enhancer
1p31.3	rs12127031	65224965	0.97	0.99	0.12	1.38	<i>RAVER2</i>	intronic	6	None	None
	rs12752552	65229299	1.00	1.00	0.23	3.01	<i>RAVER2</i>	intronic	NA	None	None
1q32.1	rs16853822	204450341	0.87	0.97	-3.78	2.51	<i>PIK3C2B</i>	intronic	4	enhancer_tss	brain (many)
	rs6668637	204452295	0.87	0.97	-1.79	1.80	<i>PIK3C2B</i>	intronic	6	enhancer_tss	brain (many)
	rs35634264	204454570	0.87	0.97	NA	NA	<i>PIK3C2B</i>	intronic	6	enhancer_tss	brain (many)
	rs12036042	204469314	0.89	0.98	2.04	9.25	5.5kb 5' of <i>PIK3C2B</i>	intergenic	4	enhancer_tss	brain (many)
	rs12031912	204476113	0.92	0.98	-0.65	2.01	9.4kb 5' of <i>MDM4</i>	intergenic	4	enhancer_tss	brain (many)
											brain (many)
	rs12028476	204476361	0.92	0.98	-2.43	3.44	9.1kb 5' of <i>MDM4</i>	intergenic	4	enhancer_tss	astrocyte_cell
	rs12039365	204488687	0.89	0.98	0.43	8.69	<i>MDM4</i>	intronic	1f	enhancer_tss	
	rs12041243	204490470	0.89	0.98	-0.87	5.68	<i>MDM4</i>	intronic	1b	enhancer_tss	
	rs12039968	204490674	0.89	0.98	0.95	2.82	<i>MDM4</i>	intronic	4	enhancer_tss	
	rs61817959	204492522	0.88	0.96	NA	0.33	<i>MDM4</i>	intronic	6	enhancer_tss	
	rs898388	204500257	0.93	0.98	-2.38	4.64	<i>MDM4</i>	intronic	4	enhancer_tss	
	rs4252697	204501383	0.91	0.98	2.06	12.99	<i>MDM4</i>	intronic	5	enhancer_tss	
	rs4252704	204506174	0.94	0.99	NA	NA	<i>MDM4</i>	intronic	NA	enhancer_tss	
	rs4252707	204508147	1.00	1.00	-0.77	0.50	<i>MDM4</i>	intronic	NA	enhancer_tss	
	rs4252733	204516918	0.89	0.96	0.63	2.14	<i>MDM4</i>	intronic	NA	enhancer_tss	
	rs11801299	204529084	0.87	0.96	-2.22	0.93	<i>MDM4</i>	intronic	6	enhancer_tss	
	rs12029692	204532323	0.87	0.96	-0.10	1.73	<i>MDM4</i>	intronic	5	enhancer_tss	
	rs6689629	204539291	0.86	0.95	0.22	4.75	<i>MDM4</i>	intronic	2b	enhancer_tss	
	rs61817460	204543579	0.87	0.96	0.99	8.78	707bp 3' of <i>MDM4</i>	intergenic	5	enhancer_tss	
1q44	rs320337	243814548	0.80	0.99	NA	1.41	<i>AKT3</i>	intronic	NA	enhancer_tss	
	rs2345993	243815373	0.93	0.98	NA	0.13	<i>AKT3</i>	intronic	NA	enhancer_tss	
	rs10803150	243822600	0.91	0.96	-2.06	1.81	<i>AKT3</i>	intronic	3a	enhancer_tss	
	rs200593524	243826003	0.84	0.96	NA	NA	<i>AKT3</i>	intronic	6	enhancer_tss	
	rs320320	243835186	0.82	1.00	1.76	9.43	<i>AKT3</i>	intronic	5	enhancer_tss	

Locus	SNP	Position	r ²	D'	GERP	CADD	Gene	Annotation	RegulomeDB	FANTOM5	Super-enhancer
	rs1843655	243837150	0.95	0.99	0.15	0.98	AKT3	intronic	5		
	rs4478795	243844576	0.95	0.99	1.44	3.72	AKT3	intronic	6		
	rs10803152	243846167	0.95	0.99	-2.68	4.91	AKT3	intronic	5		
	rs12076373	243851947	1.00	1.00	-3.01	0.11	AKT3	intronic	NA		
	rs10927059	243852079	0.82	1.00	-3.31	0.62	AKT3	intronic	5		
	rs7517921	243856420	0.82	1.00	0.00	4.91	AKT3	intronic	6		
	rs320305	243859909	0.90	0.97	-1.94	2.60	AKT3	intronic	NA		
	rs67430377	243861281	0.86	0.98	NA	NA	AKT3	intronic	6		
	rs58594024	243862702	0.93	0.97	1.33	3.13	AKT3	intronic	NA		
	rs12038981	243866855	0.88	0.97	-0.28	0.21	RP11-370K11.1	intronic	NA		
	rs12140040	243871922	0.86	0.98	-0.68	7.91	RP11-370K11.1	intronic	5		brain (several)
	rs6687181	243878518	0.90	0.97	-4.23	1.53	RP11-370K11.1	intronic	NA		
	rs35987738	243885006	0.86	0.98	NA	NA	RP11-370K11.1	intronic	5		
	rs59953491	243894953	0.90	0.97	-2.06	0.84	RP11-370K11.1	intronic	5	enhancer_promoter	brain (many)
	rs12124113	243904366	0.94	0.97	-1.04	2.96	AKT3	intronic	6		
	rs10927065	243914611	0.94	0.97	-0.48	17.06	AKT3	intronic	6		
	rs12031994	243917309	0.89	0.98	0.78	4.25	AKT3	intronic	5		
	rs10803156	243917776	0.89	0.98	0.88	2.10	AKT3	intronic	5		
	rs10927068	243923452	0.89	0.94	0.24	1.21	AKT3	intronic	NA		
	rs12047209	243954407	0.84	0.95	0.33	12.11	AKT3	intronic	NA		
2q33.3	rs35789824	209048052	0.90	-0.97	NA	NA	C2orf80	intronic	6		
	rs12995271	209048136	0.94	0.99	1.95	9.19	C2orf80	intronic	6		
	rs7583625	209048739	0.95	1.00	-2.96	5.59	C2orf80	intronic	4		
	rs10804167	209049840	0.94	-1.00	2.99	8.37	C2orf80	intronic	6		
	rs6710217	209050352	0.97	1.00	2.78	5.72	C2orf80	intronic	5		
	rs6725512	209050418	0.97	1.00	-1.88	1.50	C2orf80	intronic	5		
	rs7572263	209051586	1.00	1.00	-8.41	0.98	C2orf80	intronic	5		brain_hippocampus
	rs9646836	209055610	0.92	-0.97	NA	0.08	812bp 5' of C2orf80	intergenic	NA		
	rs148946475	209056338	0.93	-0.97	NA	NA	1.5kb 5' of C2orf80	intergenic	6		

Locus	SNP	Position	r ²	D'	GERP	CADD	Gene	Annotation	RegulomeDB	FANTOM5	Super-enhancer
	rs12995124	209057014	0.94	-0.97	0.14	0.26	2.2kb 5' of <i>C2orf80</i>	intergenic	NA		
3p14.1	rs56300148	66497714	0.92	1.00	0.52	1.20	<i>LRIG1</i>	intronic	NA		brain (many)
	rs11706832	66502981	1.00	1.00	-1.51	2.15	<i>LRIG1</i>	intronic	5		brain (many)
	rs4402869	66507444	0.86	0.98	2.88	10.79	<i>LRIG1</i>	intronic	4		brain (many)
	rs11717516	66508132	0.82	0.98	-2.74	3.59	<i>LRIG1</i>	intronic	NA		brain (many)
10q24.21	rs7100920	105640978	0.81	0.90	-2.23	3.73	1.3kb 3' of <i>OBFC1</i>	3'-UTR	6		
	rs2067832	105643134	0.81	0.90	1.06	4.01	<i>OBFC1</i>	intronic	5		
	rs58543155	105643244	0.80	0.90	-0.54	0.49	<i>OBFC1</i>	intronic	5		
	rs34300861	105643332	0.81	0.90	0.24	0.68	<i>OBFC1</i>	intronic	NA		
	rs61277100	105643352	0.81	0.90	0.24	0.70	<i>OBFC1</i>	intronic	NA		
	rs34887477	105643436	0.81	0.90	-0.47	1.14	<i>OBFC1</i>	intronic	6		
	rs34489952	105643470	0.81	0.90	NA	NA	<i>OBFC1</i>	intronic	6		
	rs4918067	105644636	0.81	0.90	-0.20	6.52	<i>OBFC1</i>	intronic	2b		
	rs4918068	105644736	0.81	0.90	3.40	9.28	<i>OBFC1</i>	intronic	4		
	rs9325507	105645622	0.82	0.90	-2.42	1.98	<i>OBFC1</i>	intronic	5		
	rs35223321	105646395	0.81	0.90	-4.73	7.23	<i>OBFC1</i>	intronic	NA		
	rs3814220	105647300	0.82	0.90	-3.03	3.50	<i>OBFC1</i>	intronic	1f		brain (several)
											brain_many
	rs199716117	105648179	0.80	0.90	NA	NA	<i>OBFC1</i>	intronic	NA		astrocyte_cell
											brain_many
	rs11191843	105648651	0.82	0.90	2.50	4.61	<i>OBFC1</i>	intronic	4		astrocyte_cell
											brain_many
	rs2273698	105649158	0.82	0.90	-5.25	3.79	<i>OBFC1</i>	intronic	5		astrocyte_cell
											brain_many
	rs11191846	105649813	0.82	0.90	1.39	4.90	<i>OBFC1</i>	intronic	3a		astrocyte_cell
											brain_many
	rs10883940	105650598	0.82	0.90	-2.41	2.78	<i>OBFC1</i>	intronic	4		astrocyte_cell
											brain_many
	rs11191847	105650626	0.82	0.90	-0.47	2.74	<i>OBFC1</i>	intronic	4		astrocyte_cell

Locus	SNP	Position	r ²	D'	GERP	CADD	Gene	Annotation	RegulomeDB	FANTOM5	Super-enhancer
	rs10883941	105650782	0.82	0.90	-0.58	3.25	OBFC1	intronic	5		brain_many astrocyte_cell
	rs11191848	105650837	0.82	0.90	-6.88	0.75	OBFC1	intronic	NA		brain_many astrocyte_cell
	rs11191849	105650880	0.82	0.90	1.84	13.52	OBFC1	intronic	NA		brain_many astrocyte_cell
	rs10883942	105651386	0.82	0.90	-1.11	0.29	OBFC1	intronic	NA		brain_many astrocyte_cell
	rs10883943	105651416	0.82	0.90	-1.44	0.67	OBFC1	intronic	6		brain_many astrocyte_cell
	rs1980653	105654164	0.82	0.90	2.36	9.03	OBFC1	intronic	5		brain_many astrocyte_cell
	rs2902639	105658588	0.84	0.91	2.21	5.28	OBFC1	intronic	6		brain_many astrocyte_cell
	rs3850671	105659387	0.83	0.91	-1.53	10.52	OBFC1	intronic	4		brain_many astrocyte_cell
	rs11598018	105661315	1.00	1.00	-0.65	1.59	OBFC1	intronic	5		brain_many astrocyte_cell
	rs10883948	105667552	0.98	1.00	1.15	3.86	OBFC1	intronic	NA		brain_many astrocyte_cell
	rs12765878	105669622	0.88	0.94	2.04	5.29	OBFC1	intronic	NA		brain_many astrocyte_cell
11q14.1	rs11191865	105672842	0.87	0.94	-1.87	1.16	OBFC1	intronic	NA		brain_many astrocyte_cell
	rs200842897	82393496	0.93	0.99	NA	NA	RP11-179A16.1	intronic	2b		None
	rs145375177	82393498	0.90	0.96	NA	NA	RP11-179A16.1	intronic	2b		None
	rs12418906	82394205	1.00	1.00	-0.09	0.38	RP11-179A16.1	intronic	3a		None
	rs11233250	82397014	1.00	1.00	-1.09	1.29	RP11-179A16.1	intronic	6		None
	rs11233251	82397293	1.00	1.00	3.09	6.29	RP11-179A16.1	intronic	6		None

Locus	SNP	Position	r ²	D'	GERP	CADD	Gene	Annotation	RegulomeDB	FANTOM5	Super-enhancer
11q21	rs11233253	82398420	1.00	1.00	-0.91	6.29	<i>RP11-179A16.1</i>	intronic	5		None
	rs569505	95730342	0.96	0.98	1.41	6.58	<i>MAML2</i>	intronic	NA		
	rs648086	95738350	0.96	0.98	-2.84	6.68	<i>MAML2</i>	intronic	6		brain (several)
	rs10765782	95745187	0.99	1.00	2.83	5.84	<i>MAML2</i>	intronic	3a	enhancer_promoter	brain (many)
	rs662766	95745273	0.99	1.00	3.00	8.43	<i>MAML2</i>	intronic	3a	enhancer_promoter	brain (many)
	rs568477	95746897	1.00	1.00	0.24	2.29	<i>MAML2</i>	intronic	3a		
14q12	rs7107785	95747337	1.00	1.00	-0.53	1.44	<i>MAML2</i>	intronic	4		
	rs926771	33246223	0.93	1.00	-3.66	0.06	<i>AKAP6</i>	intronic	6		
	rs10131032	33250081	1.00	1.00	0.67	4.36	<i>AKAP6</i>	intronic	NA		
16p13.3 (GBM)	rs2858048	122210	0.85	0.98	-3.17	0.24	<i>RHBDF1</i>	intronic	4		brain (many)
	rs2858051	122393	0.81	0.92	-2.58	0.86	<i>RHBDF1</i>	intronic	4		brain (many)
	rs2562151	122782	0.89	0.99	-1.14	9.02	<i>RHBDF1</i>	intronic	2b		brain (many)
	rs2541637	122848	0.87	0.97	-1.72	5.50	<i>RHBDF1</i>	intronic	4		brain (many)
	rs2562152	123896	1.00	1.00	-0.69	4.45	<i>RHBDF1</i>	intronic	5		brain (many)
	rs2562153	124140	0.90	1.00	-1.66	3.41	<i>RHBDF1</i>	intronic	5		brain (many)
	rs2562154	124161	1.00	1.00	-2.98	0.01	<i>RHBDF1</i>	intronic	5		brain (many)
	rs2562155	124472	0.90	1.00	-4.36	4.16	<i>RHBDF1</i>	intronic	5		brain (many)
	rs2541635	125342	0.98	1.00	0.13	3.87	<i>RHBDF1</i>	intronic	4		brain (many)
	rs2562158	125462	0.90	1.00	-2.67	1.63	<i>RHBDF1</i>	intronic	4		brain (many)
	rs2562161	125757	0.90	1.00	1.38	6.37	<i>RHBDF1</i>	intronic	2b		brain (many)
											brain_many
	rs3785288	127230	0.90	1.00	-4.04	3.35	<i>MPG</i>	intronic	4		astrocyte_cell
											brain_many
	rs3176364	127577	1.00	1.00	1.93	9.20	<i>MPG</i>	intronic	2a		astrocyte_cell
											brain_many
	rs2562162	128179	0.85	0.98	-0.45	4.82	<i>MPG</i>	5'-UTR	4		astrocyte_cell
											brain_many
	rs1013358	128954	0.99	1.00	-0.29	4.47	<i>MPG</i>	intronic	2b		astrocyte_cell

Locus	SNP	Position	r ²	D'	GERP	CADD	Gene	Annotation	RegulomeDB	FANTOM5	Super-enhancer
16p13.3 (non-GBM)	rs3751667	1004554	1.00	1.00	-11.10	0.04	LMF1	synonymous	5		brain (many)
16q12.1	rs12918457	50088068	0.82	0.91	0.32	0.45	RP11-429P3.3	intronic	6		
	rs7186889	50092291	0.90	0.95	0.24	3.83	RP11-429P3.3	intronic	NA		
	rs12599260	50093238	0.90	0.95	-1.94	3.43	RP11-429P3.3	intronic	5		
	rs1861661	50094204	0.90	0.95	-1.66	0.77	RP11-429P3.3	intronic	NA		
	rs12933325	50097444	0.91	0.96	0.52	4.49	RP11-429P3.3	intronic	1d		
	rs8046856	50098887	0.91	0.96	1.53	12.82	RP11-429P3.3	intronic	5		
	rs8052492	50099747	0.91	-0.96	-0.59	7.78	RP11-429P3.3	intronic	1f		brain (several)
	rs8051902	50099777	0.91	0.96	4.80	12.46	RP11-429P3.3	intronic	2b		brain (several)
	rs4389139	50100253	0.91	0.96	-1.21	11.91	HEATR3	intronic	3a		brain (several)
	rs1547478	50101015	0.91	0.96	0.24	14.24	HEATR3	intronic	NA		brain (several)
	rs55646814	50101526	0.91	0.97	NA	NA	HEATR3	intronic	4		brain (several)
	rs2287197	50106594	0.91	0.96	4.56	10.04	HEATR3	synonymous	5		
	rs8047504	50107635	0.92	0.96	-2.21	0.34	HEATR3	intronic	6		
	rs59059423	50108102	0.92	0.96	0.64	3.56	HEATR3	intronic	5		
	rs12932038	50108615	0.92	0.96	NA	1.10	HEATR3	intronic	6		
	rs9939688	50109100	0.92	0.96	-0.72	0.54	HEATR3	intronic	6		
	rs12931497	50109478	0.92	0.96	-9.88	0.03	HEATR3	intronic	NA		
	rs56189455	50110650	0.88	0.96	NA	NA	HEATR3	intronic	6		
	rs6416785	50111074	0.88	0.95	0.16	0.84	HEATR3	intronic	NA		
	rs7203348	50112267	0.92	0.96	0.22	1.05	HEATR3	intronic	NA		
	rs8051216	50113773	0.93	0.97	2.34	6.09	HEATR3	intronic	1f		
	rs2160570	50114505	0.93	0.97	0.16	0.73	HEATR3	intronic	6		
	rs2160571	50114555	0.92	0.97	0.22	4.55	HEATR3	intronic	6		
	rs200783489	50116682	0.80	0.95	NA	NA	HEATR3	intronic	NA		
	rs10557471	50116683	0.87	0.95	NA	NA	HEATR3	intronic	6		
	rs4591144	50116803	0.89	0.97	0.51	1.65	HEATR3	intronic	6		

Locus	SNP	Position	r ²	D'	GERP	CADD	Gene	Annotation	RegulomeDB	FANTOM5	Super-enhancer
	rs4442804	50116819	0.89	0.97	0.51	1.29	HEATR3	intronic	NA		
	rs4635343	50116999	0.94	0.97	-0.32	1.59	HEATR3	intronic	6		
	rs8047742	50117316	0.95	0.97	3.23	16.86	HEATR3	intronic	NA		
	rs877639	50118245	0.95	0.97	1.97	9.46	HEATR3	intronic	5		
	rs2080504	50119170	0.95	0.97	2.95	6.59	HEATR3	intronic	5		
	rs2287196	50120122	0.95	0.97	-11.40	0.00	HEATR3	intronic	NA		
	rs2005402	50120668	0.95	0.97	-0.71	1.47	HEATR3	intronic	NA		
	rs2356835	50120867	0.95	0.97	0.55	0.48	HEATR3	intronic	NA		
	rs2356836	50120869	0.95	0.97	0.55	1.35	HEATR3	intronic	NA		
	rs2356838	50120983	0.95	0.97	0.45	2.51	HEATR3	intronic	6		
	rs8046344	50121773	0.95	0.98	1.12	2.22	HEATR3	intronic	6		
	rs8057524	50122946	0.96	0.98	-1.42	2.66	HEATR3	intronic	NA		
	rs201019882	50123309	0.81	0.97	NA	NA	HEATR3	intronic	NA		
	rs7498242	50125145	0.95	0.98	0.15	1.04	HEATR3	intronic	NA		
	rs7190890	50125856	0.96	0.98	-1.87	0.33	HEATR3	intronic	6		
	rs113191969	50126657	1.00	1.00	NA	NA	HEATR3	intronic	5		
	rs12930079	50126691	0.99	1.00	-3.78	0.79	HEATR3	intronic	5		brain_hippocampus
	rs11642695	50127120	0.99	1.00	-4.22	0.37	HEATR3	intronic	5		brain (several) astrocyte_cell
	rs10852606	50128872	1.00	1.00	-1.07	2.66	HEATR3	intronic	NA		astrocyte_cell
	rs12926346	50130045	0.89	1.00	-1.24	0.34	HEATR3	intronic	NA		astrocyte_cell
	rs6500282	50138100	0.97	0.99	0.19	2.08	HEATR3	intronic	6		
22q13.1	rs5756908	38476579	0.95	0.99	1.58	5.49	SLC16A8	intronic	5		brain (several)
	rs4289289	38477342	0.93	0.97	-0.02	11.40	SLC16A8	missense	4		brain (several)
	rs2235573	38477930	1.00	1.00	0.12	10.84	SLC16A8	synonymous	3a		brain (several)

Data are shown for sentinel SNPs (in bold) and their proxies ($r^2 > 0.8$ in 1000 Genomes EUR Phase 1 data) with RegulomeDB scores reflecting evidence of histone marks, DNase hypersensitivity sites or transcription factor occupancy. Also indicated are genomic evolutionary rate

profiling (GERP) scores and combined annotation dependent depletion (CADD) scores as well as overlap with FANTOM5 enhancers⁵ and super-enhancers as predicted by Hnisz et al⁶. Chr, chromosome; LD, linkage disequilibrium; Pos, position; tss, transcription start site. RegulomeDB scores: 1b, eQTL + TF binding + any motif + DNase Footprint + DNase peak; 1d, eQTL + TF binding + any motif + DNase peak; 1f, eQTL + TF binding / DNase peak; 2a, TF binding + matched TF motif + matched DNase Footprint + DNase peak; 2b, TF binding + any motif + DNase Footprint + DNase peak; 3a, TF binding + any motif + DNase peak; 4, TF binding + DNase peak; 5, TF binding or DNase peak; 6, other binding or DNase peak.

Supplementary Table 6: Associations with glioma at glioma risk loci previously reported to be associated with telomere length

Locus	Reference	Source	SNP	Position	Alleles	LD (r^2/D')	All glioma		GBM glioma		Non-GBM glioma	
							<i>P</i>	Odds ratio	<i>P</i>	Odds ratio	<i>P</i>	Odds ratio
3q26.2 (<i>TERC</i>)	Codd <i>et al.</i> ¹	Telomere	rs10936599	169492101	<u>C</u> /T	-	3.17x10 ⁻⁶	1.10 (1.06-1.15)	3.22x10 ⁻⁵	1.11 (1.06-1.17)	0.01	1.07 (1.01-1.13)
		This study	rs1920116	169500487	G /A	1.00/1.00	2.25x10 ⁻⁶	1.11 (1.06-1.15)	2.68x10 ⁻⁵	1.11 (1.06-1.17)	0.01	1.07 (1.02-1.13)
5p15.33 (<i>TERT</i>)	Codd <i>et al.</i> ¹	Telomere	rs2736100	1286516	<u>C</u> /A	-	2.34x10 ⁻⁴⁵	1.29 (1.25-1.34)	1.20x10 ⁻⁵³	1.41 (1.35-1.47)	7.26x10 ⁻¹⁰	1.16 (1.10-1.21)
		This study	rs10069690	1279790	T /C	0.22/-0.80	2.71x10 ⁻⁶⁶	1.45 (1.39-1.51)	8.33x10 ⁻⁷⁴	1.61 (1.53-1.69)	1.14x10 ⁻¹⁶	1.27 (1.20-1.34)
10q24.33 (<i>OBFC1</i>)	Codd <i>et al.</i> ¹	Telomere	rs9420907	105676465	<u>C</u> /A	-	3.34x10 ⁻⁶	1.13 (1.07-1.18)	0.01	1.08 (1.02-1.15)	3.09x10 ⁻⁶	1.17 (1.09-1.25)
		This study	rs11598018	105661315	C /A	0.15/0.96	3.07x10 ⁻⁷	1.10 (1.06-1.14)	0.01	1.06 (1.01-1.11)	3.39x10 ⁻⁸	1.14 (1.09-1.20)
20q13.33 (<i>RTEL1</i>)	Codd <i>et al.</i> ¹	Telomere	rs755017	62421622	<u>G</u> /A	-	0.18	1.04 (0.98-1.10)	0.79	1.01 (0.94-1.08)	0.17	1.05 (0.98-1.13)
		This study	rs2297440	62312299	C /T	0.04/-0.27	1.60x10 ⁻⁴²	1.36 (1.30-1.42)	3.66x10 ⁻⁴⁶	1.48 (1.40-1.56)	6.90x10 ⁻¹⁰	1.20 (1.13-1.26)

Associations at telomere length loci are previously reported in Codd *et al.*, 2013¹. Reported for each locus are the association with glioma for the telomere length SNP, as well as the top SNP from the locus (within 250kb surrounding telomere length SNP) and respective LD metrics.

1. Codd, V. *et al.* Identification of seven loci affecting mean telomere length and their association with disease. *Nature Genetics* **45**, 422-427 (2013).

			GBM		Non-GBM	
Locus	SNP	RAF	Odds ratio	% risk	Odds ratio	% risk
Previously reported loci						
3q26.2	rs3772190	0.757	1.11	0.30	1.07	0.14
5p15.33	rs10069690	0.276	1.61	6.83	1.27	1.84
7p11.2	rs75061358	0.099	1.63	3.21	1.28	0.88
7p11.2	rs723527	0.573	1.25	1.84	1.08	0.23
8q24.21	rs55705857	0.057	1.27	0.46	3.39	12.91
9p21.3	rs634537	0.411	1.37	3.62	1.21	1.42
10q25.2	rs11599775	0.620	1.02	0.01	1.16	0.84
11q23.2	rs648044	0.390	0.98	0.01	1.19	1.16
11q23.3	rs12803321	0.643	1.01	0.00	1.42	4.55
12q21.2	rs1275600	0.595	1.00	0.00	1.16	0.86
12q23.33	rs12227783	0.851	1.16	0.42	1.07	0.09
15q24.2	rs77633900	0.086	1.04	0.02	1.35	1.14
17p13.1	rs78378222	0.013	2.63	1.81	2.73	2.09
20q13.33	rs2297440	0.796	1.48	3.76	1.20	0.87
TOTAL			22.30		29.00	
Loci first reported in this study						
1p31.3	rs12752552	0.870	1.22	0.67	1.11	0.20
1q32.1	rs4252707	0.220	1.07	0.12	1.19	0.84
1q44	rs12076373	0.837	0.99	0.00	1.23	0.94
2q33.3	rs7572263	0.756	1.06	0.09	1.20	0.99
3p14.1	rs11706832	0.456	1.03	0.03	1.15	0.78
10q24.33	rs11598018	0.462	1.06	0.13	1.14	0.69
11q14.1	rs11233250	0.868	1.24	0.80	0.98	0.01
11q21	rs7107785	0.479	1.00	0.00	1.16	0.89
14q12	rs10131032	0.916	1.05	0.03	1.33	1.01
16p13.3	rs2562152	0.850	1.21	0.70	1.00	0.00
16p13.3	rs3751667	0.208	1.13	0.37	1.18	0.73
16q12.1	rs10852606	0.713	1.18	0.85	1.08	0.20
22q13.1	rs2235573	0.507	1.15	0.74	1.02	0.02
TOTAL			4.53		7.28	
OVERALL			26.83		36.28	

Supplementary Table 7: Individual variance in risk associated with glioma SNPs. For each glioma risk locus, the relative risk per risk allele of the highest associated SNP is given. Risk allele frequency (RAF) is according to European samples from 1000 genomes project. Percentage (%) contributions to the familial risk of GBM and non-GBM were estimated using High-grade and low-grade glioma risk estimates of 1.76 and 1.54 respectively from the Swedish series in Scheurer *et al.*, 2010¹.

1. Scheurer, M.E. *et al.* Familial aggregation of glioma: a pooled analysis. *Am J Epidemiol* **172**, 1099-107 (2010).